

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:42:39 ; Search time 59 Seconds  
(without alignments)  
1896.421 Million cell updates/sec

Title: US-10-667-442-2

Perfect score: 2104

Sequence: 1 MGANTSRRKPPVFDENEDVNF.....NLALEQTKPDQGEDGQNNL 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2104	100.0	396	6	ABG70700 Human ser
2	2104	100.0	396	6	ABU62276 Human kin
3	2089	99.3	396	4	AB85491 Human pro
4	2089	99.3	396	5	AAE14261 Novel hum
5	2089	99.3	396	5	AAE21725 Human PKI
6	2083	99.0	396	5	AAE21725 Human PKI
7	2047	97.3	407	5	AAE14260 Novel hum
8	1500.5	71.3	327	4	AAU03504 Human pro
9	1427	67.8	404	6	ABU62277 Mouse ser
10	1425.5	67.8	403	6	ABU62278 Human ser
11	1425.5	67.8	414	4	AB65600 Novel pro
12	1425.5	67.8	414	5	ABP43807 Serine/th
13	1425.5	67.8	414	5	AAO17710 Human ser
14	1425.5	67.8	414	6	ABR58617 Human can
15	1425.5	67.8	414	7	AD338375 Human pro
16	1325	63.0	419	4	AAE65599 Novel pro
17	1321	62.8	425	4	AAE65599 Novel pro
18	1318	62.6	485	5	AAE24141 Human kin
19	1317.5	62.6	384	6	ABU62279 Mouse ser
20	1317.5	62.6	488	5	AAO17709 Murine se
21	1315	62.5	419	4	AAE38806 Human pol
22	1302	61.9	488	6	ABO14992 Human NOV
23	1285.5	61.1	713	5	ABE06090 Human NS
24	1278.5	60.8	399	5	ABE84300 Murine se
25	1259.5	59.9	375	4	AAE04371 Human kin

26	1201.5	57.1	364	4	AAU29309	Human PRO
27	1201.5	57.1	364	6	ABU58685	Human PRO
28	1201.5	57.1	364	6	ABU8233	Novel hum
29	1201.5	57.1	364	6	ABU84548	Human sec
30	1201.5	57.1	364	6	ABR66422	Human sec
31	1201.5	57.1	364	6	ABR65812	Human sec
32	1201.5	57.1	364	6	ABU99752	Human sec
33	1201.5	57.1	364	6	ABU82991	Human PRO
34	1201.5	57.1	364	6	ABU90112	Novel hum
35	1201.5	57.1	364	6	ABR68361	Human sec
36	1201.5	57.1	364	6	ABU96414	Novel hum
37	1201.5	57.1	364	6	ABU92845	Human sec
38	1201.5	57.1	364	6	ABO08922	Human sec
39	1201.5	57.1	364	6	ABO02974	Human sec
40	1201.5	57.1	364	6	ABR75128	Human sec
41	1201.5	57.1	364	6	ABR94890	Human sec
42	1201.5	57.1	364	6	ABU5863	Human PRO
43	1201.5	57.1	364	6	ABU99023	Novel hum
44	1201.5	57.1	364	6	ABU98238	Novel hum
45	1201.5	57.1	364	6	ABU91944	Novel hum

#### ALIGNMENTS

##### RESULT 1

ABG70700

ID ABG70700 standard; protein; 396 AA.

XX ABG70700;

XX 17-JAN-2003 (first entry)

XX Human serine/threonine protein kinase-like kinase.

XX Human; kinase; serine/threonine kinase; immune response; transgenic; enzyme.

XX Homo sapiens.

XX Key Location/Qualifiers

FT	Modified-site	2. .7	/label= N_myristoylation_site
FT	Modified-site	4. .7	/label= N_glycosylation_site
FT	Modified-site	5. .7	/label= Protein_kinase_C_phosphorylation_site
FT	Modified-site	6. .8	/label= Protein_kinase_C_phosphorylation_site
FT	Binding-site	29. .52	/label= Protein_kinase_C_phosphorylation_site
FT	Modified-site	33. .36	/label= Protein_kinase_ATP-binding_region
FT	Modified-site	43. .46	/label= Casein_kinase_II_phosphorylation_site
FT	Modified-site	45. .47	/label= N_glycosylation_site
FT	Modified-site	89. .92	/label= Protein_kinase_C_phosphorylation_site
FT	Modified-site	122. .124	/label= Casein_kinase_II_phosphorylation_site
FT	Active-site	142. .154	/label= Protein_kinase_C_phosphorylation_site
FT	Modified-site	193. .195	/label= Serine/threonine_protein_kinase_active_site
FT	Modified-site	194. .196	/label= Protein_kinase_C_phosphorylation_site
FT	Modified-site	197. .202	/label= Protein_kinase_C_phosphorylation_site
FT	Modified-site	212. .215	/label= N_myristoylation_site
FT	Modified-site	218. .221	/label= Casein_kinase_II_phosphorylation_site
FT	Modified-site		/label= Amidation_site

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 FT /label= Casein\_kinase\_II\_phosphorylation\_site  
 FT Modified-site 391..396  
 FT /label= N\_myristoylation\_site  
 XX US2002127683-A1.  
 XX  
 XX 12-SEP-2002.  
 XX  
 XX 09-MAR-2001; 2001US-00801876.  
 XX  
 XX 09-MAR-2001; 2001US-00801876.  
 XX  
 XX (YEJ)/ YE J.  
 XX (YANC)/ YAN C.  
 XX (DFRA)/ DI FRANCESCO V.  
 XX (BEAS)/ BEASLEY E M.

PI Ye J, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2003-0289938/02.

DR N-PSDB; ABS55499, ABS55500.

PT Novel isolated human kinase peptide useful for treating disorder  
 PT characterized by absence of, in appropriate or unwanted expression of the  
 PT kinase protein, and as immunogens to raise antibodies.

XX Claim 1; Fig 2; 174pp; English.

XX The present invention relates to the isolation of a human kinase and the  
 CC polynucleotide sequences encoding it. The human kinase of the invention  
 CC is related to the serine/threonine kinase subfamily. The gene encoding  
 CC the human kinase is located on chromosome 5. The polypeptide and  
 CC polynucleotide sequences of the invention are useful for treating a  
 CC disease or condition mediated by a human kinase. Both the polypeptide and  
 CC polynucleotide sequences are useful as models for the development of  
 CC human therapeutics, for identifying therapeutic proteins, as targets for  
 CC development of human therapeutic agents, and as query sequences to  
 CC perform a search against sequence data bases to identify other family  
 CC members of related sequences. The polypeptide is useful to raise  
 CC antibodies or to elicit another immune response, as a reagent in assays  
 CC designed to quantitatively determine levels of the protein in biological  
 CC fluids, as markers for tissues in which the corresponding protein is  
 CC preferentially expressed, in drug screening assays, in cell-based or cell  
 CC -free systems, to identify compounds that modulate kinase activity of the  
 CC protein in its natural state, or an altered form that causes the specific  
 CC disease or pathology associated with the kinase, to screen a compound for  
 CC the ability to stimulate or inhibit interaction between the kinase  
 CC protein and a molecule that normally interacts with the kinase protein,  
 CC and in pharmacogenomic analysis. The polynucleotide is useful for  
 CC monitoring the effectiveness of modulating compounds on the expression or  
 CC activity of the human kinase gene in clinical trials or in a treatment  
 CC regimen, in diagnostic assays for qualitative changes in a human kinase  
 CC nucleic acid that leads to a pathology, for testing an individual for a  
 CC genotype that while not necessarily causing a disease, nevertheless  
 CC affects the treatment modality, as antisense constructs to control human  
 CC kinase gene expression in cells, tissues and organisms, for gene therapy  
 CC in patients containing cells that are aberrant in human kinase gene  
 CC expression, and to produce transgenic animals. The present sequence  
 CC represents a human kinase related to the serine/threonine protein kinase  
 CC subfamily

XX Sequence 396 AA;

Query Match 100.0%; Score 2104; DB 6; Length 396;  
 Best Local Similarity 100.0%; Pred. NO. 8.1e-194;  
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGANTSKPVPFENEVDNFDHFEILRAIGKSGFGEVCIQKNDTKKCAKMYNKQKV 60  
 DB 1 MGANTSKPVPFENEVDNFDHFEILRAIGKSGFGEVCIQKNDTKKCAKMYNKQKV 60  
 QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRHLQNNVHFK 120

Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRHLQNNVHFK 120  
 QY 121 ETVKLFICELVVALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180  
 Db 121 ETVKLFICELVVALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180  
 QY 181 AGTKPYMAPEMFSSRKAGYSPAVDWMSLGVTAYELLGRRPYHRSSTSSKEIVHTPET 240  
 Db 181 AGTKPYMAPEMFSSRKAGYSPAVDWMSLGVTAYELLGRRPYHRSSTSSKEIVHTPET 240  
 QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQPSQLSDVQNFPMYNDINWDVAFQKRLIPGFIP 300  
 Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQPSQLSDVQNFPMYNDINWDVAFQKRLIPGFIP 300  
 QY 301 NKGRLNCDPTFLEEMILESKEPLHKKCKLAKCKEMRKCDSSQTCLLQEHLDVQKCFI 360  
 Db 301 NKGRLNCDPTFLEEMILESKEPLHKKCKLAKCKEMRKCDSSQTCLLQEHLDVQKCFI 360  
 QY 361 IFNRKVNDRDFNKRQPNLALBOTKDPQGEDGQNNNL 396  
 Db 361 IFNRKVNDRDFNKRQPNLALBOTKDPQGEDGQNNNL 396

# RESULT 2

ABU62276  
 ID ABU62276 standard; protein; 396 AA.

XX AC ABU62276;

DT 01-SEP-2003 (first entry)

DE Human kinase.

XX Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;  
 KW arteriosclerosis.

XX Homo sapiens.

OS US2003027307-A1.

PN 06-FEB-2003.

XX 26-SEP-2002; 2002US-00254869.

XX 09-MAR-2001; 2001US-00801876.

PR (APPL-) APPLERA CORP.

XX Ye J, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2003-492035/58.

DR N-PSDB; ACA62840, ACA62841.

XX New isolated human kinase proteins, useful for treating disorders  
 PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis  
 PT or psoriasis), or for development of human therapeutics and diagnostic  
 PT compositions.

XX Claim 1; Fig 2A; 185pp; English.

XX The invention relates to a new isolated human kinase peptide. The human  
 CC kinase peptide and nucleic acid molecules are useful in the development  
 CC of human therapeutics and diagnostic compositions. The peptides are  
 CC useful for treating disorders (e.g. cancers, inflammations,  
 CC arteriosclerosis or psoriasis) characterised by an absence of,  
 CC inappropriately, or unwanted expression of the kinase protein. These  
 CC molecules are particularly useful as models for developing human  
 CC therapeutic targets, identifying therapeutic proteins, or serving as  
 CC targets for the development of human therapeutic agents that modulate  
 CC kinase activity in cells and tissues that express the kinase. The  
 CC peptides are also useful for raising antibodies or eliciting an immune  
 CC response; as a reagent (including the labelled reagent) in assays



## RESULT 4

AAE14261  
ID AAE14261 standard; protein; 396 AA.  
XX  
AC AAE14261;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Novel human protein (NHP) kinase #4.  
XX  
KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;  
KW medical disorder; mental; biological; physiological; chemotherapeutic.  
XX  
OS Homo sapiens.  
XX  
PN WO200181557-A2.  
XX  
PD 01-NOV-2001.  
XX  
PF 24-APR-2001; 2001WO-US013149.  
XX  
PR 25-APR-2000; 2000US-0199499P.  
PR 01-MAY-2000; 2000US-0201227P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;  
PI WPI: 2002-034442/04.  
DR N-PSDB; AAD23679.  
XX  
XX New nucleic acid molecules encoding new human proteins, useful in  
PT diagnosis, drug screening, clinical trial monitoring, treatment of  
PT physiological disorders, and cosmetic or nutraceutical applications.  
XX  
PS Claim 7; Page 43; 44pp; English.  
XX  
CC The invention relates to novel human protein (NHP) kinases and their  
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as  
CC reagents in assays for screening compounds that can be used as  
CC pharmaceutical reagents useful in the therapeutic treatment of mental,  
CC biological and medical disorders, and also as chemotherapeutic agents,  
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is  
CC useful for diagnosis, drug screening, clinical trial monitoring, the  
CC treatment of physiological disorders or diseases, and cosmetic and  
CC nutraceutical applications. NHP DNA is also useful for the identification  
CC of coding sequence and the mapping of a unique gene to a particular  
CC chromosome. NHP DNA is further useful as hybridization probes for  
CC screening libraries and assessing gene expression patterns, and also for  
CC the detection of mutant NHPs or inappropriately expressed NHPs for  
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present  
CC sequence is novel human protein (NHP) kinase which is similar to  
CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-  
CC dependent kinases related to the invention  
XX  
SQ Sequence 396 AA;  
Query Match 99.3%; Score 2089; DB 5; Length 396;  
Best Local Similarity 99.5%; Pred. No. 2.3e-192;  
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MGANTSKPVPFDENDVDFHFEILRAIGKSGFGEVCIQKNDTKKCMKMYNKKQCV 60  
Db 1 MGANTSKPVPFDENDVDFHFEILRAIGKSGFGEVCIQKNDTKKCMKMYNKKQCV 60  
Qy 61 ERNEVRNVFQELQIMQGLEHFFLVNLYWSFQDEDMFVVDLLGGDLRYHLQNVHFK 120  
Db 61 ERNEVRNVFQELQIMQGLEHFFLVNLYWSFQDEDMFVVDLLGGDLRYHLQNVHFK 120  
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPNILLDEHGHVHTDFTNIAAMLPRETOITTM 180  
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPNILLDEHGHVHTDFTNIAAMLPRETOITTM 180

Qy 181 AGTKPYMAPENFSSRKAGYGFVDMWSLGVYATVYELLGRPPYHRSSTSSKEIVHTPET 240  
Db 181 AGTKPYMAPENFSSRKAGYGFVDMWSLGVYATVYELLGRPPYHRSSTSSKEIVHTPET 240  
Qy 241 TVVTYPSAWSOEMVSLKLLLEPNPDQRFSSQSDVQNPFPYNDINWDVAFQKRLIPGPI 300  
Db 241 TVVTYPSAWSOEMVSLKLLLEPNPDQRFSSQSDVQNPFPYNDINWDVAFQKRLIPGPI 300  
Qy 301 NKGRINCDDPTFELESEMILESPLHKKKRLAKKXKMDKCDSSQTCLLQEHLDVQKKEFI 360  
Db 301 NKGRINCDDPTFELESEMILESPLHKKKRLAKKXKMDKCDSSQTCLLQEHLDVQKKEFI 360  
Qy 361 IFNREKVNDRDNFKQPNLALBQTKDPOGEDQNNNL 396  
Db 361 IFNREKVNDRDNFKQPNLALBQTKDPOGEDQNNNL 396

## RESULT 5

AAE21725  
ID AAE21725 standard; protein; 396 AA.  
XX  
AC AAE21725;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE Human PKIN-20 protein.  
XX  
KW Human; kinase; enzyme; PKIN-20 protein; immune system disorder; anaemia;  
KW acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease;  
KW asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease;  
KW AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma;  
KW leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder;  
KW Down's syndrome; gene therapy; protein therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 13..300 /note= "Protein kinase domain"  
FT Domain 23..300 /note= "Protein kinase domain"  
FT Domain 23..281 /note= "Eukaryotic protein kinase domain"  
FT Domain 25..270 /note= "Protein kinase domain"  
FT Domain 25..268 /note= "Protein kinase domain"  
XX  
PN WO200218557-A2.  
XX  
XX 07-MAR-2002.  
XX  
XX 31-AUG-2001; 2001WO-US027219.  
XX  
XX 31-AUG-2000; 2000US-0229873P.  
XX 08-SEP-2000; 2000US-0231357P.  
XX 14-SEP-2000; 2000US-0232654P.  
XX 22-SEP-2000; 2000US-0234902P.  
XX 29-SEP-2000; 2000US-0236499P.  
XX 06-OCT-2000; 2000US-0238389P.  
XX 13-OCT-2000; 2000US-0240542P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
PI Bandman O, Nguyen DB, Wallia NK, Hafalia AJA, Yao MG, Gandhi AR;  
PI Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;  
PI Thornton M, Elliott VS, Lu Y, Leon CH, Au-Young J, Tang YT;  
PI Azimzal Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG;  
PI Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;  
PI Burford N;  
XX  
XX WPI: 2002-329769/36.  
DR



DR N-PSDB; AAD34317.  
XX  
PT New human kinases, useful for diagnosing, treating or preventing immune  
PT system disorders (e.g. Crohn's disease), neurological disorders (e.g.  
PT epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia  
PT or lymphoma).  
XX  
PS Claim 75; Page 184-185; 218pp; English.  
XX  
CC The present invention relates to human kinases (PKIN) and polynucleotides  
CC encoding such proteins. PKIN sequences of the invention are useful for  
CC diagnosing, treating or preventing disorders associated with aberrant  
CC expression of PKIN, particularly immune system disorders (e.g. acquired  
CC immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,  
CC anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-  
CC Tooth disease or seizures), cell proliferative disorders (e.g. cancers  
CC such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma),  
CC and developmental disorders (e.g. Down's syndrome). They are also used in  
CC gene therapy and protein therapy. The present sequence is human PKIN-20  
XX protein.  
XX  
SQ Sequence 396 AA;  
  
Query Match 99.3%; Score 2089; DB 5; Length 396;  
Best Local Similarity 99.5%; Pred. No. 2.3e-192;  
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
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DB 1 MGANTSRKPPVFDENEDVDFEILRAIGKSGFGEVCIQKNDTKKCKAMKYNKQKV 60  
  
QY 61 ERNEVRNVKELQIMQGLEPFLVNIWYSFQDEDMFVVDLLGGDLRYHLOQNVHFK 120  
DB 61 ERNEVRNVKELQIMQGLEPFLVNIWYSFQDEDMFVVDLLGGDLRYHLOQNVHFK 120  
  
QY 121 ETVKLFICELVMDYLQNR1IHRDMKPDN1LLDEGHVH1TDFN1AAMLPRETQ1TTM 180  
DB 121 ETVKLFICELVMDYLQNR1IHRDMKPDN1LLDEGHVH1TDFN1AAMLPRETQ1TTM 180  
  
QY 181 AGTKPYMAPSPSRKAGSFAVDWWSLGVATYELLGRPPYHRSSTSSKSEIVHTFET 240  
DB 181 AGTKPYMAPSPSRKAGSFAVDWWSLGVATYELLGRPPYHRSSTSSKSEIVHTFET 240  
  
QY 241 TVVTYSAQSWQSVLLKLEPNPDORFQSDVQNPFPYMDINWDVAFQKRLIPGFI 300  
DB 241 TVVTYSAQSWQSVLLKLEPNPDORFQSDVQNPFPYMDINWDVAFQKRLIPGFI 300  
  
QY 301 NKGRNLCDPTFEELMILESPLHKKKRLAKKEKMRKCDSSQTCILQEHLDVQKEFI 360  
DB 301 NKGRNLCDPTFEELMILESPLHKKKRLAKKEKMRKCDSSQTCILQEHLDVQKEFI 360  
  
QY 361 IFNREKVNDRFNKRPNALAEQTKDQGEDGQNNL 396  
DB 361 IFNREKVNDRFNKRPNALAEQTKDQGEDGQNNL 396  
  
RESULT 6  
AAM50334  
ID AAM50334 standard; protein; 396 AA.  
AC AAM50334;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Human 14911 protein kinase.  
XX  
KW Protein kinase; human; signal transduction; lung cancer; colon cancer;  
KW brain cancer; breast cancer; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 2.7

PT Modified-site 4.7  
PT Modified-site 5.7  
PT Domain 23.281  
PT Peptide 29.37  
PT Modified-site 43.46  
PT Modified-site 45.47  
PT Modified-site 89.92  
PT Modified-site 122.124  
PT Active-site 142.154  
PT Modified-site 193.195  
PT Modified-site 197.202  
PT Modified-site 212.215  
PT Modified-site 218.221  
PT Modified-site 230.233  
PT Modified-site 230.232  
PT Domain 282.301  
PT Modified-site 391.396  
PT  
XX WO200181589-A2.  
XX  
XX 01-NOV-2001.  
XX  
XX 25-APR-2001; 2001WO-US013785.  
XX  
XX 25-APR-2000; 2000US-0199391P.  
XX 15-JUN-2000; 2000US-00593927.  
XX (WILL-) MILLENNIUM PHARM INC.  
XX  
XX Meyers R, Hunter JJ;  
XX WPI; 2002-041408/05.  
XX N-PSDB; AAI70704.  
XX  
XX Novel protein kinase nucleic acid molecules and the encoded proteins for  
XX diagnosing and treating cellular proliferative, bone, immune,  
XX cardiovascular, liver, pain or metabolic disorders and identifying  
XX modulators.  
XX  
XX Claim 4(d); Fig 1A-B; 115pp; English.  
XX  
XX The present sequence is that of a novel human protein kinase, designated  
XX 14911. This protein kinase plays a role in, or functions in, the  
XX transduction of signals for cell proliferation, differentiation and  
XX apoptosis, modulating the activity of one or more proteins involved in  
XX cellular growth or differentiation. 14911 molecules are overexpressed in  
XX some tumour cells, where they may inappropriately propagate either cell  
XX proliferation or cell survival signals. The invention provides methods  
XX for the diagnosis and treatment of cancer, including breast cancer, brain  
XX and especially lung cancer (claimed), and methods for evaluating the  
XX efficacy of treatment. 14911 polypeptides can be produced by cultivation  
XX of claimed host cells, and used in claimed methods of identifying 14911  
XX modulator compounds. 14911 binding partners are used in claimed methods  
XX of identifying subjects at risk of cancer or cellular proliferation  
XX and/or differentiation disorders. A claimed method of treating cancer or

/notes="N-myristoylated"  
4.7  
/notes="Asn is N-glycosylated"  
5.7  
/notes="O-phosphorylated by protein kinase C"  
23.281  
/label="Protein\_kinase\_domain"  
29.37  
/notes="protein kinase ATP-binding region signature"  
43.46  
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45.47  
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89.92  
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122.124  
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218.221  
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230.233  
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230.232  
/notes="O-phosphorylated by protein kinase C"  
282.301  
/label="Protein\_kinase\_C-terminal\_domain"  
391.396  
/notes="N-myristoylated"

CC a cellular proliferation and/or differentiation disorder, especially  
CC lung, colon, brain and breast cancer, uses a small molecule, peptide,  
CC phosphopeptide, anti-14911 antibody, a 14911 polypeptide or its variant.  
CC Other disorders that may be diagnosed/treated include those associated  
CC with bone metabolism, autoimmune diseases, cardiovascular disorders,  
CC liver disorders, viral diseases, pain and metabolic disorders  
XX  
SQ Sequence 396 AA;

Query Match 99.0%; Score 2083; DB 5; Length 396;  
Best Local Similarity 99.2%; Pred. No. 8.6e-192;  
Matches 393; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGDLRYHLQQNVHFK 120  
DB 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGDLRYHLQQNVHFK 120  
QY 121 ETVKLFICELVWALDYLNQRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETIQITM 180  
DB 121 ETVKLFICELVWALDYLNQRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETIQITM 180  
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAELLRRRPHYHRSSTSSKEIVHTPET 240  
DB 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAELLRRRPHYHRSSTSSKEIVHTPET 240  
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRPSQLSDVQNPFPYMDINWDVAFQKRLIPGPIP 300  
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRPSQLSDVQNPFPYMDINWDVAFQKRLIPGPIP 300  
QY 301 NKGRNLCDPTPELEEMILESPLHKKKRLAKKEDMKDCSSQTCLLQEHLDVSKKEFI 360  
DB 301 NKGRNLCDPTPELEEMILESPLHKKKRLAKKEDMKDCSSQTCLLQEHLDVSKKEFI 360  
QY 361 IFNREKVRNDFNKRQPNLALEQTQKPDQGEDGQNNNL 396  
DB 361 IFNREKVRNDFNKRQPNLALEQTQKPDQGEDGQNNNL 396

RESULT 7  
AAE14260  
ID AAE14260 standard; protein; 407 AA.  
XX  
AC AAE14260;  
XX  
XX 07-MAR-2002 (first entry)  
XX  
XX Novel human protein (NHP) kinase #3.  
XX  
XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
KW Gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;  
KW medical disorder; mental; biological; physiological; chemotherapeutic.  
XX  
XX Homo sapiens.  
XX  
XX WO200181557-A2.  
XX  
XX 01-NOV-2001.  
XX  
XX 24-APR-2001; 2001WO-US013149.  
XX  
XX 25-APR-2000; 2000US-0199499P.  
PR 01-MAY-2000; 2000US-0201227P.  
XX  
XX (LEXI-) LEXICON GENETICS INC.  
XX  
XX Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;  
PI WPI: 2002-034442/04.  
DR N-PSDB; AAD23678.

XX New nucleic acid molecules encoding new human proteins, useful in  
PT diagnosis, drug screening, clinical trial monitoring, treatment of  
PT physiological disorders, and cosmetic or nutraceutical applications.  
XX  
PS Claim 5; Page 41-42; 44pp; English.

XX The invention relates to novel human protein (NHP) kinases and their  
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as  
CC reagents in assays for screening compounds that can be used as  
CC pharmaceutical reagents useful in the therapeutic treatment of mental,  
CC biological and medical disorders, and also as chemotherapeutic agents  
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is  
CC useful for diagnosis, drug screening, clinical trial monitoring, the  
CC treatment of physiological disorders, or diseases, and cosmetic and  
CC nutraceutical applications. NHP DNA is also useful for the identification  
CC of coding sequence and the mapping of a unique gene to a particular  
CC chromosome. NHP DNA is further useful as hybridisation probes for  
CC screening libraries and assessing gene expression patterns, and also for  
CC the detection of mutant NHPs or inappropriately expressed NHPs for  
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present  
CC sequence is novel human protein (NHP) kinase which is similar to  
CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-  
CC dependent kinases related to the invention

XX Sequence 407 AA;

Query Match 97.3%; Score 2047; DB 5; Length 407;  
Best Local Similarity 98.7%; Pred. No. 2.6e-188;  
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGDLRYHLQQNVHFK 120  
DB 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGDLRYHLQQNVHFK 120  
QY 121 ETVKLFICELVWALDYLNQRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETIQITM 180  
DB 121 ETVKLFICELVWALDYLNQRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETIQITM 180  
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAELLRRRPHYHRSSTSSKEIVHTPET 240  
DB 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAELLRRRPHYHRSSTSSKEIVHTPET 240  
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRPSQLSDVQNPFPYMDINWDVAFQKRLIPGPIP 300  
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRPSQLSDVQNPFPYMDINWDVAFQKRLIPGPIP 300  
QY 301 NKGRNLCDPTPELEEMILESPLHKKKRLAKKEDMKDCSSQTCLLQEHLDVSKKEFI 360  
DB 301 NKGRNLCDPTPELEEMILESPLHKKKRLAKKEDMKDCSSQTCLLQEHLDVSKKEFI 360  
QY 361 IFNREKVRNDFNKRQPNLALEQTQKPDQGEDGQ 392  
DB 361 IFNREKVRNDFNKRQPNLALEQTQKPDQVNTGQ 392

RESULT 8

AAU03504  
ID AAU03504 standard; protein; 327 AA.  
XX  
XX AAU03504;  
XX  
XX 12-SEP-2001 (first entry)  
DT  
DE Human protein kinase #4.  
XX  
XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;  
KW metabolic disorder; immune related disease; neurological disorder;  
KW neurodegenerative disorder; inflammatory disorder; infectious disease;



Db 121 EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHTDNIATVILKGSEKASS 180

QY 180 MAGTKPYMAPEMPS--SRKAGYSPAVDMWSLGVATYELLGRPRPHYHRSSTSSKEIVHT 237

Db 181 MAGTKPYMAPEVQVYVDGPGYSYFVDMWSLGVATYELLGRWRPYEIHSAITPIDILNM 240

QY 238 PETTVVYPSANQEMVSLKLLLEPNPDRFSDVQNFQFYMNDINWDAVPEKELIIG 297

Db 241 FKVERVHYSTWCEGMVSLKLLTKDPSRSLSSLDIOSMTYLDAMNWDVAFKALMPG 300

QY 298 FIPNKGRLNCDPTFELEEMILESPLHKKKKRIAK--KEKDMRKCDSSQTCLLQEHLDVQ 356

Db 301 FVFNKGRNCDPTFELEEMILESPLHKKKKRIAKHRSRSTKDSCLPLNGHLQOCLETVR 360

QY 357 KEFIIIFNREKVRDNFKRQPNLALQTKDPQGEDGQNNL 396

Db 361 KEFIIIFNREKLRQ-----QGHGQLSDL 384

RESULT 10

ABU62278

ID ABU62278 standard; protein; 403 AA.

AC ABU62278;

XX

DT 01-SEP-2003 (first entry)

XX

DE Human serine/threonine protein kinase #1.

XX

KW Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;

KW arteriosclerosis.

XX

OS Homo sapiens.

XX

PN US2003027307-A1.

XX

PD 06-FEB-2003.

XX

PF 26-SEP-2002; 2002US-00254869.

XX

PR 09-MAR-2001; 2001US-00801876.

XX

PA (APPL-) APPLERA CORP.

XX

PI Ye J, Yan C, Di Francesco V, Beasley EM;

XX

DR WPI; 2003-492035/58.

XX

PT New isolated human kinase proteins, useful for treating disorders

PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis

PT or psoriasis), or for development of human therapeutics and diagnostic

PT compositions.

XX

PS Disclosure; Fig 2B; 185pp; English.

XX

CC The invention relates to a new isolated human kinase peptide. The human

CC kinase peptide and nucleic acid molecules are useful in the development

CC of human therapeutics and diagnostic compositions. The peptides are

CC useful for treating disorders (e.g. cancers, inflammations,

CC arteriosclerosis or psoriasis) characterised by an absence of,

CC inappropriate, or unwanted expression of the kinase protein. These

CC molecules are particularly useful as models for developing human

CC therapeutic targets, identifying therapeutic proteins, or serving as

CC targets for the development of human therapeutic agents that modulate

CC kinase activity in cells and tissues that express the kinase. The

CC peptides are also useful for raising antibodies or eliciting an immune

CC response; as a reagent (including the labelled reagent) in assays

CC designed to quantitatively determine levels of the protein (or its

CC binding partner or ligand) in biological fluids; or as markers for

CC tissues in which the corresponding protein is preferentially expressed.

CC The agents identified are useful for treating a subject with a disorder

CC mediated by kinase pathway. The present sequence represents the amino

CC acid sequence of the human serine/threonine protein kinase #1

XX SQ Sequence 403 AA;

Query Match 67.8%; Score 1425.5; DB 6; Length 403;

Best Local Similarity 68.2%; Pred. No. 2.1e-128;

Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

QY 1 MGNTSRKPPVDEDEDVDFHFEILRAIGSGFGEVCIVQKDPTEKGMKMYMKQKCV 60

Db 1 MGNHSHKPPVDEDEEYVDFHFEILRAIGSGFGEVCIVQKDRTKGMYMKMKQKCI 60

QY 61 ERNEVNVFKELIQMOGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120

Db 61 ERDEVNVFRELQIQMOGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFE 120

QY 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDNIAMLPRETQITM 180

Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHTDNIATVVKGAERASM 180

QY 181 AGTKPYMAPEMPS--SRKAGYSPAVDMWSLGVATYELLGRPRPHYHRSSTSSKEIVHTF 238

Db 181 AGTKPYMAPEVQVYVDGPGYSYFVDMWSLGVATYELLGRWRPYEIHSAITPIDILNM 240

QY 239 ETTVVTYPSANQEMVSLKLLLEPNPDRFSDVQNFQFYMNDINWDAVPEKELIIG 298

Db 241 KVERVHYSTWCKGNVALLKLLTKDPSRVSLLDIQSVPLADMNWDVAFKALMPGF 300

QY 299 FPNKGRNCDPTFELEEMILESPLHKKKKRIAK--KEKDMRKCDSSQTCLLQEHLDVQ 357

Db 301 FVFNKGRNCDPTFELEEMILESPLHKKKKRIAKHRSRSTKDSCLPLNGHLQOCLETVR 360

QY 358 KEFIIIFNREKVRDNFKRQPNLALQTKDPQ-----EDGQNNL 396

Db 361 KEFIIIFNREKLRQ-----QGHGQLSDL 403

RESULT 11

ABU65600

ID AAB65600 standard; protein; 414 AA.

XX

AC AAB65600;

XX

DT 27-MAR-2001 (first entry)

XX

DE Novel protein kinase, SEQ ID NO: 125.

XX

KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;

KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;

KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;

KW immune disorder; cardiovascular disease; neurodegenerative disease;

KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;

KW inflammatory pelvic disease; multiple sclerosis; psoriasis.

XX

OS Homo sapiens.

XX

PN WO2000073469-A2.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US014842.

XX

PR 28-MAY-1999; 99US-0136503P.

XX

PA (SUGB-) SUGEN INC.

XX

PI Plowman GD, Martinez R, Whyte D, Sudersanam S;

XX

DR WPI; 2001-032161/04.

XX

DR N-PSDB; AAF44625.

XX

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and

PT treating immune-related diseases and disorders, cardiovascular disease,

PT neurodegenerative diseases and/or cancers.

XX Claim 10; Fig 1; 310pp; English.

XX The present sequence is a novel protein kinase. The novel protein kinases

CC and the nucleic acids that encode them may be used in the treatment and

CC diagnosis of diseases associated with inappropriate kinase expression

CC such as immune-related diseases and disorders, cardiovascular disease,

CC neurodegenerative diseases and/or cancers. The nucleic acids and

CC complementary sequences may also be used as DNA probes in diagnostic

CC assays. The kinase polypeptides may be used as antigens in the production

CC of antibodies of kinase expression and activity. Anti-kinase antibodies

CC and kinase antagonists may also be used to down regulate kinase

CC expression and activity. Diseases related to kinase expression and

CC activity include rheumatoid arthritis, atherosclerosis, autoimmune

CC disorders, complications of organ transplantation, myocardial infarction,

CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-

CC stress related disorders, chronic inflammatory bowel disease, chronic

CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,

CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive

CC disorders

XX Sequence 414 AA;

Query Match 67.8%; Score 1425.5; DB 4; Length 414;  
Best Local Similarity 68.2%; Pred. No. 2.2e-128;  
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy 1 MGNTSRKPPVDEEDVNFDPHPIILRAIGKSGFGEVCIQKNTKKMCAMKYNKQCV 60  
Db 1 MGGNHSHKPPVDEEDVNFDPHPIILRAIGKSGFGEVCIQKNTKKMCAMKYNKQCI 60

Qy 61 ERNEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPKE 120  
Db 61 ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPTE 120

Qy 121 ETVKLFICELVMDLYLQNRRIHRDKMKNPNDLLDEHGHVHTDFTNIAAMLPRTOITTM 180  
Db 121 GTVKLYICELALALEYLQRYHIIHRDKPNNDLLDEHGHVHTDFTNIAATVKGABRASSM 180

Qy 181 AGTKPYMAPEMFS--SRKAGYSPAVDWSIGVTAYELLGRPRPHYHRSSTSSKEIVHTP 238  
Db 181 AGTKPYMAPEVQVYMDRGPGYSPVDWWSIGITAYELLGRWRPYEHTSVTPIDEILNMP 240

Qy 239 ETTVVITYPSAWSQBMVSLKLLKJLEPNPDQRFPSQLSDVQNFPPYMDINWDVAFQRLIPGF 298  
Db 241 KVERVHYSSWCKGVALLRKLLTKDPESRVSSLDIQSVPYLADMDWDAVFKALMPGP 300

Qy 299 IPNKGRLNCDPTFELEEMILSKPLHKKKRLAK-KEKDMRKCDSSQTCLLQHLDSVQK 357  
Db 301 VPNGRLNCDPTFELEEMILSKPLHKKKRLAKNRSDGTGKSCPLNGHLQHCLETVRE 360

Qy 358 EFIIFNREKVRDNFKRQPNLALEQTKDPOG---EDGQNNNL 396  
Db 361 EFIIFNREKRRQGGQSLLDTSRGGGQAQSKLQDGCNNNL 403

RESULT 12

ABP43807

ID ABP43807 standard; protein; 414 AA.

XX AC ABP43807;

XX DT 26-FEB-2003 (first entry)

XX DE Serine/threonine kinase.

XX KW Neuroprotective; immunomodulator; cancer; chromosome 4p16.1-p14;

XX KW cytosolic; anti-inflammatory; gene therapy; nutritional supplement;

XX KW wound; burn; ulcer; Alzheimer's disease; Huntington's disease;

XX KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;

XX KW vulnary.

OS Homo sapiens.

XX WO200231111-A2.

XX 18-APR-2002.

XX 11-OCT-2001; 2001WO-US027760.

XX 12-OCT-2000; 2000US-00687527.

XX (HYSB-) HYSQ INC.

XX Tang YT, Liu C, Zhou P, Auandi V, Zhang J, Zhao QA, Ren P;  
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX N-PSDB; ABQ61051.

XX WPI; 2002-426278/45.

XX New polypeptides and their encoded proteins, useful as nutritional  
PT sources or supplements, or in gene therapy, particularly for treating  
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
PT inflammation.

XX Claim 20; SEQ ID # 710; 357pp + Sequence Listing; English.

XX The invention relates to 446 newly isolated polynucleotide sequences. The  
CC activity of polynucleotides of the invention may be described as,  
CC vulnary, neuroprotective, immunomodulator, cytosolic and anti-  
CC inflammatory. Compositions comprising nucleic acids of the invention are  
CC useful for treating a mammalian subject, or as nutritional sources or  
CC supplements. These are useful in gene therapy, particularly for treating  
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
CC inflammation. The nucleic acids and polypeptides are also useful in  
CC diagnostic and research methods. The sequences given in records ABP43544-  
CC ABP43989 represent polypeptides encoded by polynucleotides of the  
CC invention. NOTE: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

XX Sequence 414 AA;

Query Match 67.8%; Score 1425.5; DB 5; Length 414;  
Best Local Similarity 68.2%; Pred. No. 2.2e-128;  
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy 1 MGNTSRKPPVDEEDVNFDPHPIILRAIGKSGFGEVCIQKNTKKMCAMKYNKQCV 60  
Db 1 MGGNHSHKPPVDEEDVNFDPHPIILRAIGKSGFGEVCIQKNTKKMCAMKYNKQCI 60

Qy 61 ERNEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPKE 120  
Db 61 ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPTE 120

Qy 121 ETVKLFICELVMDLYLQNRRIHRDKMKNPNDLLDEHGHVHTDFTNIAAMLPRTOITTM 180  
Db 121 GTVKLYICELALALEYLQRYHIIHRDKPNNDLLDEHGHVHTDFTNIAATVKGABRASSM 180

Qy 181 AGTKPYMAPEMFS--SRKAGYSPAVDWSIGVTAYELLGRPRPHYHRSSTSSKEIVHTP 238  
Db 181 AGTKPYMAPEVQVYMDRGPGYSPVDWWSIGITAYELLGRWRPYEHTSVTPIDEILNMP 240

Qy 239 ETTVVITYPSAWSQBMVSLKLLKJLEPNPDQRFPSQLSDVQNFPPYMDINWDVAFQRLIPGF 298  
Db 241 KVERVHYSSWCKGVALLRKLLTKDPESRVSSLDIQSVPYLADMDWDAVFKALMPGP 300

Qy 299 IPNKGRLNCDPTFELEEMILSKPLHKKKRLAK-KEKDMRKCDSSQTCLLQHLDSVQK 357  
Db 301 VPNGRLNCDPTFELEEMILSKPLHKKKRLAKNRSDGTGKSCPLNGHLQHCLETVRE 360

Qy 358 EFIIFNREKVRDNFKRQPNLALEQTKDPOG---EDGQNNNL 396  
Db 361 EFIIFNREKRRQGGQSLLDTSRGGGQAQSKLQDGCNNNL 403

RESULT 13  
 AAO17710  
 ID AAO17710 standard; protein; 414 AA.  
 XX  
 AC AAO17710;  
 XX  
 DT 20-AUG-2002 (first entry)  
 XX  
 DE Human serine-threonine protein kinase #2.  
 XX  
 KW Human; serine-threonine protein kinase; cancer; diabetes; obesity;  
 KW central nervous system disorder; inflammation; gene therapy; COPD;  
 KW neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;  
 KW antidiabetic; antiasthmatic; antidepressant; anorectic;  
 KW antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;  
 KW enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233056-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-EP011892.  
 XX  
 PR 16-OCT-2000; 2000US-0240097P.  
 PR 30-JUL-2001; 2001US-0308096P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Koehler RH;  
 XX  
 DR WPI; 2002-435534/46.  
 XX  
 PT New human serine-threonine protein kinase and encoding polynucleotides,  
 PT useful for diagnosing, treating and preventing central nervous system  
 PT disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).  
 XX  
 PS Disclosure; Fig 8; 135pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of a  
 CC human serine-threonine protein kinase. The sequences can be used in the  
 CC diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma  
 CC or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or  
 CC traumatic brain injury), diabetes, eating disorders (e.g. obesity,  
 CC anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and  
 CC chronic obstructive pulmonary disease (COPD). The present sequence is a  
 CC human serine-threonine protein kinase  
 XX  
 SQ Sequence 414 AA;  
 Query Match 67.8%; Score 1425.5; DB 5; Length 414;  
 Best Local Similarity 68.2%; Pred. No. 2.2e-128;  
 Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;  
 QY 1 MGATSKRPVDFEDNEDVDFHFLRAIGKSGFVCIVQKNDTKKCMKMYNKQKV 60  
 DB 1 MGNHSHKPPVDFEDNEDVDFHFLRAIGKSGFVCIVQKNDTKKCMKMYNKQKI 60  
 QY 61 ERNEVRNVPELQIMQGLRHPFLVNLVYSFQDEDMFVVDLLGGDLRLHLOQNVHFK 120  
 DB 61 ERDEVRNVFRELQIMQGLRHPFLVNLVYSFQDEDMFVVDLLGGDLRLHLOQNVHTE 120  
 QY 121 ETVKLFICELVMALDYLNQRIHRDKMPKNILDERGHVHITDFTNIAMLPRETQITTM 180  
 DB 121 GTVKLYICELALALEYLRVHIIHRDKPKNILDERGHVHITDFTNIAATVVKGAERASSM 180  
 QY 181 AGTKPYNAPEMPS--SRKAGYSFADVMSLGVYAYELLACRRPYHTRSTSSKEIVHTP 238  
 DB 181 AGTKPYNAPEVQVYMDRPGYSYFVDVMSLGVYAYELLACRRPYHTRSTSSKEIVHTP 240  
 QY 239 ETTVVTVYPSAWSQEMVSLKLLKLEPNPQRPQPSQLSDVQNFPMYNDINWDAVFQKRLIPGF 298

Db 241 KVERVHYSTWCKGMVALLRKULTKDPESRVSSLLHDIOSVPLADNMWDVAFKALMPGF 300  
 QY 299 IPNKGRLNCDDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK 357  
 Db 301 VFNKGRNCDDPTFELEEMILESPLHKKKKRLAKRSRGTGKSCPLNGLHQCLFVRE 360  
 QY 358 EPIIFNREKVRNDFNKRQPNLALQETKDPQG-----EDGQNNNL 396  
 Db 361 EPIIFNREKLRQGGSQLDTPDSRGGGQAQSKLQDGCNNNL 403

RESULT 14  
 ABR58617  
 ID ABR58617 standard; protein; 414 AA.  
 XX  
 AC ABR58617;  
 XX  
 DT 09-JUL-2003 (first entry)  
 XX  
 DE Human cancer related protein SEQ ID NO:274.  
 XX  
 KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;  
 KW heart disease; atherosclerosis; endometriosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025138-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-US029560.  
 XX  
 PR 17-SEP-2001; 2001US-0323469P.  
 PR 20-SEP-2001; 2001US-0323887P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 08-FEB-2002; 2002US-0355145P.  
 PR 08-FEB-2002; 2002US-0355257P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB;  
 PI Zlotnik A;  
 XX  
 DR WPI; 2003-354600/33.  
 DR N-PSDB; ACC72764.  
 XX  
 PT New genes that are up-regulated or down-regulated in cancers, useful as  
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
 PT therapeutic targets for screening drugs for treating these diseases.  
 XX  
 Claim 12; Page 749; 767pp; English.  
 The present invention describes an isolated nucleic acid molecule, which  
 comprises the sequence of any of the genes that are up-regulated or down-  
 regulated in specific cancers (e.g. about 1031 genes up-regulated in  
 acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer  
 related gene nucleotide sequences which encode the proteins given in  
 ABR58521 to ABR58709. Also described: (1) determining the presence or  
 absence of a pathological cell in a patient; (2) an expression vector  
 comprising a nucleic acid molecule described above; (3) a host cell  
 comprising the vector; (4) an isolated polypeptide, which is encoded by  
 the nucleic acid; (5) an antibody that specifically binds the polypeptide  
 of (4); (6) specifically targeting a compound to a pathological cell in a  
 patient by administering to the patient the antibody above; and (7) a  
 drug screening assay. The nucleic acid is useful as diagnostic markers or  
 therapeutic targets. In particular, the nucleic acid is useful for  
 diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
 bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
 pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
 atherosclerosis and endometriosis. The nucleic acid is also useful in  
 drug screening, particularly for identifying agents for treating these

CC pathologies  
XX Sequence 414 AA;  
SQ

Query Match 67.8%; Score 1425.5; DB 6; Length 414;  
Best Local Similarity 68.2%; Pred. No. 2.2e-128;  
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

QY 1 MGANTSRKPPVFDENEDVNFDPHETLRAIGKSGFGEVCIVQKNDTKKCMKYNKQCV 60  
DB 1 MGNHSHKPPVFDENEVNFDFHQLLRAIGKSGFGEVCIVQKNDTKKCMKYNKQCV 60  
QY 61 ERNEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHTE 120  
DB 61 ERNEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHTE 120  
QY 121 ETVKLFICELVMDLYLQNRQIHRDKMPDNLDEHGHVHTDFNTAAMLPRQTITM 180  
DB 121 GTVKLYICELALALEYLQRYHIIHRDKMPDNLDEHGHVHTDFNTAATVVKGAERASSM 180  
QY 181 AGTKPYMAPEMFS--SRKGAGYSFVDMWSLGVTAHELLRGRPRYHRSSTSSKEIVHTP 238  
DB 181 AGTKPYMAPVQVYMDRGPGYSFVDMWSLGVTAHELLRGRPRYHRSVTPIDEILNMF 240  
QY 239 ETTVVTPSAWSQEMVSLKLLBPNDPQRFSDVQNFQFYMNDINWDVAFQKRLIPGF 298  
DB 241 KVERVHYSSWCKGNVALLKLLTKDPESRVSSLDIQSVPLADMNWDVAFKALMPGF 300  
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DB 361 EPIIFNREKVRNDFNKPQNLALQTKDPQG----EDGQNNNL 403

RESULT 15  
ADE38375  
ID ADE38375 standard; protein; 414 AA.  
XX  
AC ADE38375;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human protein 3703 amino acid sequence.  
XX  
KW tumorigenic disorder; angiogenic disorder; aberrant gene expression;  
KW aberrant protein activity; cytostatic; antithyroid; antidiabetic;  
KW ophthalmological; cancer; breast cancer; colon cancer; lung cancer;  
KW prostatic cancer; Grave's disease; diabetic retinopathy; protein 3703.  
XX Homo sapiens.  
OS  
XX WO2003065006-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 30-JAN-2003; 2003WO-US002588.  
XX  
PR 31-JAN-2002; 2002US-0353600P.  
PR 15-MAR-2002; 2002US-0364517P.  
PR 09-APR-2002; 2002US-0371075P.  
PR 10-APR-2002; 2002US-0371507P.  
PR 16-APR-2002; 2002US-0372984P.  
PR 19-APR-2002; 2002US-0374194P.  
PR 24-MAY-2002; 2002US-0382995P.  
PR 31-MAY-2002; 2002US-0385023P.  
PR 14-JUN-2002; 2002US-0388533P.  
PR 17-JUN-2002; 2002US-0389395P.  
PR 25-JUN-2002; 2002US-0391324P.  
PR 15-JUL-2002; 2002US-0395944P.  
PR 22-JUL-2002; 2002US-0397726P.

PR 13-AUG-2002; 2002US-0403046P.  
PR 22-AUG-2002; 2002US-0405155P.  
PR 27-AUG-2002; 2002US-0406361P.  
PR 25-OCT-2002; 2002US-0421195P.  
PR 12-NOV-2002; 2002US-0425456P.  
PR 19-NOV-2002; 2002US-0427626P.  
PR 10-DEC-2002; 2002US-0432122P.  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX Hunter JJ, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES;  
PI Williamson MW, Rudolph-Owen LA;  
FI  
XX WPI; 2003-646176/61.  
DR  
XX N-PSDB; ADE38374.  
DX  
FT Treating subject having tumorigenic disorder or angiogenic disorder  
FT caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic  
FT acid, by administering a modulator.  
XX  
PS Disclosure; SEQ ID NO 36; 454pp; English.  
XX  
CC This invention relates to a novel method of treating a human subject  
CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant  
CC gene expression or activity of an isolated protein, by administering a  
CC modulator. The modulator may have cytostatic, antithyroid, antidiabetic  
CC or ophthalmological activity. The method is useful for treating a subject  
CC having a tumorigenic or angiogenic disorder, in particular for treating  
CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic  
CC cancer) and, for example, Grave's disease and diabetic retinopathy. The  
CC present sequence is the amino acid sequence of the novel isolated human  
CC protein 3703 of the invention.  
XX  
SQ Sequence 414 AA;

Query Match 67.8%; Score 1425.5; DB 7; Length 414;  
Best Local Similarity 68.2%; Pred. No. 2.2e-128;  
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

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QY 121 ETVKLFICELVMDLYLQNRQIHRDKMPDNLDEHGHVHTDFNTAAMLPRQTITM 180  
DB 121 GTVKLYICELALALEYLQRYHIIHRDKMPDNLDEHGHVHTDFNTAATVVKGAERASSM 180  
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DB 181 AGTKPYMAPVQVYMDRGPGYSFVDMWSLGVTAHELLRGRPRYHRSVTPIDEILNMF 240  
QY 239 ETTVVTPSAWSQEMVSLKLLBPNDPQRFSDVQNFQFYMNDINWDVAFQKRLIPGF 298  
DB 241 KVERVHYSSWCKGNVALLKLLTKDPESRVSSLDIQSVPLADMNWDVAFKALMPGF 300  
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DB 301 VPNGRLNCDPTFELEEMILESPLHKKKRLAKNRSDGTDKSCPLNGHLQHCLETVRE 360  
QY 358 EPIIFNREKVRNDFNKPQNLALQTKDPQG----EDGQNNNL 396  
DB 361 EPIIFNREKVRNDFNKPQNLALQTKDPQG----EDGQNNNL 403

Search completed: June 25, 2004, 10:49:07  
Job time : 62 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:55:12 ; Search time 2826 Seconds  
(without alignments)  
15691.910 Million cell updates/sec

Title: US-10-667-442-1  
Perfect score: 1485  
Sequence: 1 ccatggagcgaacattca.....taaaaaaaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 1008

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_estl.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_eston.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gssi.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	968	65.2	1927	11 AK042599	AK042599 Mus muscu
2	968	65.2	2477	11 AK044474	AK044474 Mus muscu
3	968	65.2	3766	11 AK036266	AK036266 Mus muscu
4	710.6	47.9	893	10 BG036777	BG036777 60228692

5	555.2	37.4	3439	11 AK082468	AK082468 Mus muscu
6	553.6	37.3	1245	29 AY406286	AY406286 Mus muscu
7	540.8	36.4	1245	29 AY406284	AY406284 Homo sapi
8	533.8	35.9	1245	29 AY406285	AY406285 Pan trogl
9	494.4	33.3	2161	11 AK046439	AK046439 Mus muscu
10	466	31.4	829	13 BU156055	BU156055 AGENCOURT
11	455.2	30.7	836	13 BU412592	BU412592 603155332
12	426.8	28.7	869	10 BG033516	BG033516 602302120
13	421.6	28.4	1072	12 BM908009	BM908009 AGENCOURT
14	417.8	28.1	724	14 CB522564	CB522564 UI-M-GHO-
15	388.8	26.2	711	14 CA320851	CA320851 UI-M-FWO-
16	375.2	25.3	1003	13 BU146507	BU146507 AGENCOURT
17	372.4	25.1	995	13 BX401698	BX401698 BX401698
18	372.4	25.1	648	13 BV726568	BV726568 BV726568
19	365.6	24.6	664	10 BF472636	BF472636 UI-M-BH3-
20	364	24.5	1045	13 BX384945	BX384945 BX384945
21	361	24.3	1063	13 BQ925566	BQ925566 AGENCOURT
22	356.4	24.0	1201	13 BX416707	BX416707 BX416707
23	352.6	23.7	773	12 B1917132	B1917132 603181546
24	348.2	23.4	868	14 CP736437	CP736437 UI-M-HD0-
25	345.4	23.3	643	10 BB629092	BB629092 BB629092
26	341.2	23.0	667	10 BB642433	BB642433 BB642433
27	341	23.0	948	13 BX342288	BX342288 BX342288
28	340	22.9	862	10 BB567816	BB567816 601340485
29	333.2	22.4	1000	12 BG824303	BG824303 602727322
30	320.2	21.6	1055	13 BX384918	BX384918 BX384918
31	314.8	21.2	769	13 BQ571307	BQ571307 UI-M-FC0-
32	305.6	20.6	449	12 BQ44851	BQ44851 UI-M-EH0P
33	294.4	19.8	851	14 CA454976	CA454976 AGENCOURT
34	290.8	19.6	725	14 CD578874	CD578874 UI-M-GMO-
35	289.2	19.5	869	12 BG719068	BG719068 602699189
36	280.6	18.9	626	14 CA327599	CA327599 UI-M-PYO-
37	255.4	17.2	438	9 AI430616	AI430616 meo9f10.y
38	254.2	17.1	451	14 W65887	W65887 meo9f10.r1
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40	250	16.8	600	13 BX855511	BX855511 BX855511
41	247	16.6	578	12 BM934086	BM934086 UI-M-CG0P
42	245.2	16.5	1201	13 BX362859	BX362859 BX362859
43	238.8	16.1	778	14 CB520836	CB520836 UI-M-GHO-
44	233.8	15.7	639	13 BU320918	BU320918 603498113
45	233.4	15.7	365	10 BE947841	BE947841 UI-M-BH3-

#### ALIGNMENTS

#### RESULT 1

#### AK042599

#### LOCUS

#### DEFINITION

#### ACCESION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### MEDLINE

#### PUBMED

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### MEDLINE

#### PUBMED

AK042599 1927 bp mRNA linear HTC 19-SEP-2003  
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length  
enriched library, clone:A730009C22 product:SIMILAR TO SERINE  
THREONINE KINASE 32 homolog (Homo sapiens), full insert sequence.

AK042599 GI:26335202

HTC, CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, K., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159



REFERENCE  
AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

REFERENCE  
AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

REFERENCE  
AUTHORS

5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 1927)

JOURNAL  
REFERENCE  
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.  
Direct Submission

## JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/

## FEATURES

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841 ATATGATGATATAAATCTGGGATGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTC 900  
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## ORIGIN

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Matches 1218; Conservative 0; Mismatches 245; Indels 43; Gaps 6;  
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DB 714 AAG 773  
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JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Genome Res. 10 (10), 1617-1630 (2000)  
20493374  
11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaehiwa, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer

## TITLE

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

5

Nature 409, 685-690 (2001)  
The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

## TITLE

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Nature 420, 563-573 (2002)  
6 (bases 1 to 3766)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.

## TITLE

## JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/.

## FEATURES

## source

Location/Qualifiers  
1. 3766  
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243..1439  
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## ORIGIN

Query Match 65.2%; Score 968; DB 11; Length 3766;  
Best Local Similarity 80.9%; Pred. No. 2.5e-172; Indels 43; Gaps 6;  
Matches 1218; Conservative 0; Mismatches 245;  
QY 1 CCATGGGAGCGAACACTTCAAGAAACACCAACAGTGTGTGATGAAATGAAGATGTCAACT 60  
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QY 61 TTGACCACTTTGAAATTTTGGAGGCAATTTGGAAAGGCGAGTTTGGGGAGGTCTGCAATG 120  
DB 301 TTGACCACTTTGAAATTTTGGAGGCAATTTGGAAAGGCGAGTTTGGGGAGGTCTGCAATG 360  
QY 121 TACAGAGAAATGATACCAAGAGAGTGTGCGCAATGAATGATGATGATGATGATGATGATG 180  
DB 361 TCGGAGAGAAATGATACCAAGAGAGTGTGCGCAATGAATGATGATGATGATGATGATGATG 420  
QY 181 TGGAGCGCAATGAAGTGAAGAAATGTCTCAAGAACTCCAGATCATGACGAGGTCTGGAGC 240  
DB 421 TGGAGCGCAATGAAGTGAAGAAATGTCTCAAGAACTCCAGATCATGACGAGGTCTGGAGC 480  
QY 241 ACCCTTTCTGTTAATTTTGGTATTTCTTCCAGATGAGGAGGAGACATGTTTCATGGTGG 300  
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QY 301 TGGAGCTCTGCTGGTGGTGGAGACCTGCGTTATCCTGCAACAGAACGTCCTCAATCAAG 360  
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QY 361 AAGAAACAGTGAAGCTCTTTCATCTGTGAGTGGTCTGATGCTGCTGCTGCTGCTGCTGCTG 420  
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 1294 ACTTGAATAATGTAATGATATATTTTCAAAAAAGGAGGACCAACACAGTGA----- 1345  
 1561 ACTTGAATAATGTAATGATAGTCTTTCGAAGTGTGAGGAGCTCTGCGAGCACTCTGCGAGCAGGA 1620  
 1346 -----AGGTCCTGGGCTGAGCTCTTCAAGTGTGAGGAGCTCTGCGAGCACTCTGCGAGCAGGA 1397  
 1621 GAGGAAGAGAGGCTGCTGAGCTCTTCAAGTGTGAGGAGCTCTGCGAGCACTCTGCGAGCAGGA 1680  
 1398 GATCTAGAGCAAGTCACTTAGGCACTTTCTGCTGCTTTTACTTTATTTATCTAAATGAGAG 1457  
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 1458 GGTAT 1463  
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RESULT 4  
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 LOCUS  
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 mRNA sequence.  
 BG036777  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC <http://mgi.nci.nih.gov/>  
 Unpublished (1999)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM10041 row: h column: 24  
 High quality sequence stop: 764.

## FEATURES

## source

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 5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
 insert size 2.5 kb and normalized to 10<sup>7</sup> 5. This is a  
 primary library enriched for full-length clones and  
 constructed using the Cap-trapper method (Carninci, in  
 preparation). Library constructed by M. Brownstein  
 (NHGRI/NHGRI, National Institutes of Health). Note: this  
 is a NIH\_MGC Library."

## ORIGIN

Query Match 47.9%; Score 710.6; DB 10; Length 893;  
 Best Local Similarity 97.3%; Pred. No. 1e-123;  
 Matches 733; Conservative 0; Mismatches 19; Indels 1; Gaps 1;  
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 770 TCTTAAAAAGCTACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCA 829  
 546 TCTTAAAAAGCTACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCA 605  
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 606 GAACTTCCGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 665

QY 890 AGTTTTCATTCCTAATAAGGAGGCTGAATTGTGATCCTACCTTTTGAACTTCGAGGAAT 949  
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QY 950 GATTTTGGAGTCCAAACCTCTACATAGAAAAA 982  
 Db 726 GA-TTTGGGTCCAAACCTCTACATAGAAAAA 757

RESULT 5  
 AK082468  
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 DEFINITION  
 Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length  
 enriched library, clone:C230053G02 product:serine threonine kinase  
 32, full insert sequence.

ACCESSION  
 AK082468.1 GI:26349720  
 VERSION  
 H7C; CAP trapper.  
 KEYWORDS  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 10349636

REFERENCE  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20493974  
 11042159

REFERENCE  
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--394-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861

REFERENCE  
 4 The RIKEN Genome Exploration Research Group Phase II Team and the  
 PANTOM Consortium  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)

TITLE  
 The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 3439)

REFERENCE  
 5 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
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 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.

TITLE  
JOURNAL

## COMMENT

## FEATURES

## Source

## CDS

## polyA\_signal

## polyA\_site

## ORIGIN

Query Match 37.4%; Score 555.2; DB 11; Length 3439;  
 Best Local Similarity 69.9%; Pred. No. 1.1e-94;  
 Matches 781; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

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 Db 609 CCTTCTCTGGTAAACCTATGTTGTTCTTCCAGGATGAGGAGAGACATGTTTCATGGTGGT 668

Direct Submission  
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/.

Location/Qualifiers  
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/db\_xref="FANTOM DB:C230053G02"

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evidence: ELASTN, 99%, match=1955)"

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3439

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genomic survey sequence.  
ACCESSION AY406285  
VERSION AY406285.1 GI:39762259  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
1 (bases 1 to 1245)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
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Best Local Similarity 68.2%; Pred. No. 1.6e-90;  
Matches 762; Conservative 0; Mismatches 347; Indels 9; Gaps 2;  
QY 3 ATGGAGCGAACACTTCAAGAAACCAACAGTGTGTTGATGAAATGAGATGTCACTTT 62  
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QY 483 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGAGACACAGATTTACCACTG 542

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Db 721 AAGGTGAGGCGGTGCTCACTACTCTCCACGCTGTGTCAGGAGGAGTGTGCTGAGG 780

QY 777 AAGCTACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTC 836

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QY 957 GAGTCMAAACCTCTACATAAGAAAGAAAAGCCCTCTGGCAAGAA---GGAGAGGATATG 1013

Db 961 GAATCCAGCCACTTTCACAAAAGAGAGAGCGGTTGGCAAGACAGATCCAGGATGCG 1020

QY 1014 AGGAATGCGATTTCTTCAGACATGTCTTCTTCAAGAGCCTTGACTCTGTCCAGAG 1073

Db 1021 ACGAAGGACAGCTGCCCGCTGAATGAGACACCTGCGAGCAGTGTTCGAGAGCTGTCCGGAAG 1080

QY 1074 GAGTTCTAATTTTCAACAGAGAAAAGCTTAACAGGGA 1111

Db 1081 GAATTCATCATATTCAACAGAGAGAGCTCAGGAGGCA 1118

## RESULT 9

AK046439

LOCUS

DEFINITION

AK046439

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

AK046439 2161 bp mRNA linear HTC 20-SBP-2003  
Mus musculus adult male corpora quadrigenina cDNA, RIKEN  
full-length enriched library, clone:B230385A21 product:inypotheical  
serine/threonine protein kinase, full insert sequence.

AK046439  
AK046439.1 GI:26338088  
HTC; CAP trapper

Mus musculus (house mouse)  
Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)  
99279253

10349636  
2  
REFERENCE  
AUTHORS  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL  
Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE  
20499374  
PUBMED  
11042159  
REFERENCE  
3  
AUTHORS  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hara, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
TITLE  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL  
Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE  
20530913  
PUBMED  
11076861  
REFERENCE  
4  
AUTHORS  
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE  
Functional annotation of a full-length mouse cDNA collection  
JOURNAL  
Nature 409, 685-690 (2001)  
REFERENCE  
5  
AUTHORS  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL  
Nature 420, 563-573 (2002)  
REFERENCE  
6  
AUTHORS  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
COMMENT  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/  
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1. 2161  
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ORIGIN  
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Matches 734; Conservative 0; Mismatches 346; Indels 12; Gaps 2;  
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QY 90 GGGAAAGGCAGTTTTCGGGAGGTCTGCATTTGTACAGAAATGATATCAAGAAAGATGTGC 149  
DB 410 GGGAAAGGCAGCTTTTGGCAAGGTGTGCATCGTCAGAGCGGACACAGAGAAAGATGTAC 469  
QY 150 GCATCAAGTACATGATGAAATGAAGTGGTGGAGCGCAATGAAGTGAAGATGCTTC 209  
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DB 530 CGGAGCTGGAGATCTTACAGGAATCGAGCATGTCTTCTGTGTGAACCTCTGTACTCC 589  
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QY 330 TATCACTGCACAGAACCTCCACTTTCAGAGGAACAGTGAAGTCTTCTCATCTGTGAG 389  
DB 650 TACCACCTACAGCAGAAATGTCCAGTTCCTCAGAGGACACAGTGAAGCTGTACATCTGTGAG 709  
QY 390 CTGGTCATGCGCCCTGACCTACCTGCAAGAACCCAGCGCATCATTCACAGGATATGAAGCCT 449  
DB 710 ATGGCCCTGGCCCTGGACCTACCTGCGTAGCCACACATCATCCACAGAGATGTCAAGCCT 769  
QY 450 GACAAATTTTACTTGACGAAACATGGGCGAGTGCACATACAGATTTCAACATTTGCTGGCG 509  
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QY 510 ATGCTGCCAGGAGACACAGATTTACCATGCTGGGACCAAGCTTACATGTCACCTTACATGGCACCT 569  
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QY 804 CGATTTTCTCAGTATCTGATGTCACAGAACTTCCCGTATATGATGATATAAATGCGGAT 863
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RESULT 10
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DEFINITION AGENCOURT_7970922 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6163821
5', mRNA sequence.
ACCESSION BUI56055
VERSION BUI56055.1 GI:22669587
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ARCC/DCRP/DTP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13519 row: o column: 22
High quality sequence start: 7
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Average insert size 2 kb. Library constructed by Life
Technologies."

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Query Match 31.4%; Score 466; DB 13; Length 829;

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DB 251 CCATGGGAGCGAACAACATTTCAAGAAAAACACAGAGTTTGTGATGAAAAATGAAGATGTCAACT 310
QY 61 TTGACCACTTTTGAATTTTGGAGCCATTGGGAAAGGAGGAGTTTGGGAGGCTCTGCATTG 120
DB 311 TTGACCACTTTTGAATTTTGGAGCCATTGGGAAAGGAGGAGTTTGGGAGGCTCTGCATTG 370
QY 121 TACAGAGAAATGATACCAAGAGAGATGTGCGCAATGAAGTACATGATATAACAAAAAGTGGC 180
DB 371 TACAGAAATATGATACCAAGAGAGATGTAGCGCAATGAAGTACATGATATAACAAAAAGTGGC 430
QY 181 TGGAGCGCAATGAAAGTGAATATGCTTCAAGGAACCTCCAGATCATGCAAGGCTCTGGAGC 240
DB 431 TGGAGCGCAATGAAAGTGAATATGCTTCAAGGAACCTCCAGATCATGCAAGGCTCTGGAGC 490
QY 241 ACCCTTCTCTGTTAAATTTGTGTTATCTCTTCAAGATGAGGAAGACATGTTTCATGTGGTGG 300
DB 491 ACCCTTCTCTGTTAAATTTGTGTTATCTCTTCAAGATGAGGAAGACATGTTTCATGTGGTGG 550
QY 301 TGGACCTCTCTGCTGGTGGAGACCTGCGTTATCACTCCAAAGAGAGTCCACTTCAAGG 360
DB 551 TGGACCTCTCTGCTGGTGGAGACCTGCGTTATCACTCCAAAGAGAGTCCACTTCAAGG 610
QY 361 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTTCATGCGCTGAGTCCCTGCACTACCTGCAAGACC 420
DB 611 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTTCATGCGCTGAGTCCCTGCACTACCTGCAAGACC 670
QY 421 AGCGCATCATTCACAGGAGATGATGAAGCTCGACATATTTTACTTCAGCAACATG 474
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RESULT 11
LOCUS BUI412592 836 bp mRNA linear EST 29-NOV-2002
DEFINITION BUI412592 CSEQRBL05 Gallus gallus cDNA clone ChEST168p8 5', mRNA
sequence.
ACCESSION BUI412592
VERSION BUI412592.1 GI:25905263
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 836)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source Location/Qualifiers
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/organism="Gallus gallus"
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/clone="ChEST168p8"
/sex="Female"
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## RESULT 13

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DEFINITION 5', mRNA sequence.  
ACCESSION BM908009  
VERSION BM908009.1 GI:19358388  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1072)  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12767 row: c column: 18  
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cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

FEATURES  
source

Query Match 28.4%; Score 421.6; DB 12; Length 1072;  
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DB 59 ATGGGAGCGAACAACCTTCAAGAAACCAACCAAGTCTTTGATGAAATGAAGATGTCAACTTT 118  
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QY 123 CAGAAGATGATACCAAGAGATGTGGCAATGCAATGATGATGATGATGATGATGATGATGATGAT 182  
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QY 243 CCTTCTCGGTAAATTTGGTATTCCTCCAGATGAGGAGCAACATGTTTCATGTTGGTG 302  
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QY 303 GACCTCTCTGCTGGTGGAGCACCTGCGTATTACCTGCAACAGAACGTCCTCAAGGAA 362

## ORIGIN

Query Match 28.4%; Score 421.6; DB 12; Length 1072;  
Best Local Similarity 69.4%; Pred. No. 2.2e-69;  
Matches 602; Conservative 0; Mismatches 257; Indels 8; Gaps 2;  
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DB 299 CCTTCTCGGTCAATCTGTGTACTCTTCCAGATGAGGAGCAACATGTTTCATGTTGGTG 358  
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FEATURES  
source

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Db 359 GACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGACAGAGAAATGTCATTTTCACAG 418  
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QY 835 TCCCTATATGAATGATATAAATGCGG 861  
Db 899 TCCCTATCTGTCGACATGAACCGG 925

CB522564 724 bp mRNA linear EST 09-JUL-2003  
UI-M-GH0-Seq-a-14-0-UI-r1 NIH\_BMAP\_GH0 Mus musculus cDNA clone  
IMAGE:5842871 5', mRNA sequence.

CB522564  
EST. GI:29355919

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mouseefl.html>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. .724

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/strain="C57BL/6"

/db\_xref="taxon:10090"





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 22:20:22 ; Search time 500 Seconds  
(without alignments)

13605.835 Million cell updates/sec

Title: US-10-667-442-1

Perfect score: 1485

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1485	100.0	1485	9	US-09-801-876B-1
2	1485	100.0	1485	13	US-10-667-442-1
3	1485	100.0	1485	15	US-10-254-869-1
4	1228.6	82.7	1281	15	US-10-410-764-100
5	1188.2	80.0	1594	13	US-10-362-892-44
6	1188.2	80.0	1594	13	US-10-182-243-1
7	1188.2	80.0	1594	16	US-10-288-798-44
8	1185.2	79.9	1191	9	US-09-841-683-10
9	1184.6	79.8	1191	16	US-10-410-764-102
10	1162.6	78.3	1675	9	US-09-841-683-12
11	1160.6	78.2	1224	9	US-09-841-683-8
12	1029.4	69.3	2063	16	US-10-108-260A-231
13	672.8	45.3	678	13	US-10-276-774-239
14	656.2	44.2	711	9	US-09-841-683-6

15	655.2	44.1	678	9	US-09-841-683-4	Sequence 4, Appli
16	540.8	36.4	3224	13	US-10-342-887-1782	Sequence 1782, Ap
17	540.8	36.4	3224	13	US-10-172-118-1782	Sequence 1782, Ap
18	540.8	36.4	3224	15	US-10-161-803-40	Sequence 40, Appl
19	540.8	36.4	3224	15	US-10-354-358-35	Sequence 35, Appl
20	516.4	34.8	3244	13	US-10-206-915-571	Sequence 571, App
21	516.4	34.8	3244	13	US-10-199-670-571	Sequence 571, App
22	516.4	34.8	3244	13	US-10-201-858-571	Sequence 571, App
23	516.4	34.8	3244	13	US-10-205-890-571	Sequence 571, App
24	516.4	34.8	3244	13	US-10-208-024-571	Sequence 571, App
25	516.4	34.8	3244	13	US-10-201-853-571	Sequence 571, App
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29	516.4	34.8	3244	13	US-10-176-914-571	Sequence 571, App
30	516.4	34.8	3244	13	US-10-176-915-571	Sequence 571, App
31	516.4	34.8	3244	13	US-10-176-484-571	Sequence 571, App
32	516.4	34.8	3244	13	US-10-183-014-571	Sequence 571, App
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38	516.4	34.8	3244	13	US-10-194-460-571	Sequence 571, App
39	516.4	34.8	3244	13	US-10-194-463-571	Sequence 571, App
40	516.4	34.8	3244	13	US-10-194-484-571	Sequence 571, App
41	516.4	34.8	3244	13	US-10-195-884-571	Sequence 571, App
42	516.4	34.8	3244	13	US-10-195-886-571	Sequence 571, App
43	516.4	34.8	3244	13	US-10-196-744-571	Sequence 571, App
44	516.4	34.8	3244	13	US-10-196-755-571	Sequence 571, App
45	516.4	34.8	3244	13	US-10-196-757-571	Sequence 571, App

#### ALIGNMENTS

#### RESULT 1

US-09-801-876B-1  
; Sequence 1, Application US/09801876B  
; Patent No. US20020127683A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160  
; CURRENT APPLICATION NUMBER: US/09/801.876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1485  
; TYPE: DNA  
; ORGANISM: Human  
US-09-801-876B-1

Query Match	100.0%;	Score	1485;	DB	9;	Length	1485;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1485;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	CCATGGGAGCGAACACCTTCAAGAAAAACCCACAGTGTGTGATGAAAAATGAAGATGTCAACT	60				
Qy	61	TTGACCACTTTGAAATTTTGGAGCCATTTGGAAAGGCAGTTTGGGGAGGTCTGCATTG	120				
Db	61	TTGACCACTTTGAAATTTTGGAGCCATTTGGAAAGGCAGTTTGGGGAGGTCTGCATTG	120				
Qy	121	TACAGAGAATGATACCAAGAGATGCGCAATGAAGTACATCAATAAACAAGTGC	180				
Db	121	TACAGAGAATGATACCAAGAGATGCGCAATGAAGTACATCAATAAACAAGTGC	180				
Qy	181	TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATCGGGTCTGGAGC	240				



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241 ACCCTTTCTGGTGAATTTGTGTATTTCTTCAAGATGAGGAGACATGTTTCATGGTG 300  
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## RESULT 2

US-10-667-442-1  
; Sequence 1, Application US/10667442  
; Publication No. US20040043466A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160DIV II  
; CURRENT APPLICATION NUMBER: US/10/667,442  
; CURRENT FILING DATE: 2003-09-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1485  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-667-442-1

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 121 TACAGAAAGATGATACCAAGAGATGTGCGCAATGAAATGATGATGATGATGATGATG 180  
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DB 241 ACCCTTTCTGGTGAATTTGTGTATTTCTTCAAGATGAGGAGACATGTTTCAATG 300  
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DB 361 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGTGCTGAGCTGAGCTGAGGAC 420  
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Db 1141 TGGAAACAAACCAAGACCCACAGGTGAGGATGGTCAGATACAACTTGTAAAGCCTC 1200
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Db 1321 CAAAAAGGAGCAGCAACACAGTGAAGGCTCTGGGCTGAGCTCTGGAAAGTCAATTC 1380
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RESULT 4
US-10-410-764-100
; Sequence 100, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; FILE REFERENCE: NP103-0520NM
; CURRENT APPLICATION NUMBER: US/10/410, 764
; CURRENT FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2000-09-01
; PRIOR FILING DATE: 2000-09-01
; PRIOR FILING DATE: 2003-01-24
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; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)...(1239)
US-10-410-764-100
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 47 CCATGGGAGCGCAACACTTCAAGAAACCCACAGATGTTTGTAGTGAATGAAGATGTCAACT 106
QY 61 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGCAGTTTGGGAGGTTCTGCATTG 120
Db 107 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGCAGTTTGGGAGGTTCTGCATTG 166
QY 121 TACAGAAAGATGATACCAAGAGATGCGGCAATGAAGTACATGAATATAAAGAGTGGC 180
Db 167 TACAGAAAGATGATACCAAGAGATGCGGCAATGAAGTACATGAATATAAAGAGTGGC 226
QY 181 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCAAGGTCTGGAGC 240
Db 227 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCAAGGTCTGGAGC 286
QY 241 ACCCTTCTCTGTTAAATTTTGGTATTTCTTCCAAAGATGAGGAGACATGTTTCATGTTGG 300
Db 287 ACCCTTCTCTGTTAAATTTTGGTATTTCTTCCAAAGATGAGGAGACATGTTTCATGTTGG 346
QY 301 TGGACCTCTCTGTTGGTGGAGACCTGCGTTATCCTTCAAGAACTCCAGATCATGCAAGGTCTGGAGC 360
Db 347 TGGACCTCTCTGTTGGTGGAGACCTGCGTTATCCTTCAAGAACTCCAGATCATGCAAGGTCTGGAGC 406
QY 361 AAGAAACAGTGAAGCTCTTCACTGTGAGTGGTCAATGGCCCTGCACTACCTGCAAGAAC 420
Db 407 AAGAAACAGTGAAGCTCTTCACTGTGAGTGGTCAATGGCCCTGCACTACCTGCAAGAAC 466
QY 421 AGCGCATCATTCACAGGAGATGAGCCTGCAATATTTTACTTCAAGCAATGCGGACG 480
Db 467 AGCGCATCATTCACAGGAGATGAGCCTGCAATATTTTACTTCAAGCAATGCGGACG 526
QY 481 TGCACATCAGAGATTTCAACATTTGCTGCGATGCTGCCAGGAGAGACACAGATTATCACCA 540
Db 527 TGCACATCAGAGATTTCAACATTTGCTGCGATGCTGCCAGGAGAGATACAGATTATCACCA 586
QY 541 TGGCTGGCAACCAAGCTTTACATGGCACTGAGATGTTTCAAGTCTCAAGAAAGAGGAGGCT 600
Db 587 TGGCTGGCAACCAAGCTTTACATGGCACTGAGATGTTTCAAGTCTCAAGAAAGAGGAGGCT 646
QY 601 ATTCTTTGCTGTTGACTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG 660
Db 647 ATTCTTTGCTGTTGACTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG 706
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Publication No. US20030207299A1  
GENERAL INFORMATION:  
APPLICANT: BANDMAN, Olga; NGUYEN, Damiel B;  
APPLICANT: WALIA, Narinder K.; HAPALIA, April J.A.;  
APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;  
APPLICANT: GURURAJAN, Rajagopal; DING, Li;  
APPLICANT: PATTURSON, Chandra; YUB, Henry;  
APPLICANT: BAUGHN, Maria R.; TRIBOULEY, Catherine M.;  
APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;  
APPLICANT: LU, Yan; ISON, Craig H.;  
APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;  
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;  
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
APPLICANT: LU, Dyoung Aina M.; LAL, Preeti G.;  
APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;  
APPLICANT: KERNERY, Liam; POLICKY, Jennifer L.;  
APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil  
TITLE OF INVENTION: HUMAN KINASES  
FILE REFERENCE: PI-0209 USA  
CURRENT APPLICATION NUMBER: US/10/288,798  
CURRENT FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: PCT/US01/27219  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/240,542  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/238,389  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/236,499  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 60/234,902  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US 60/232,654  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: US 60/231,357  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: US 60/229,873  
PRIOR FILING DATE: 2000-08-31  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PERL Program  
SEQ ID NO 44  
LENGTH: 1594  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20030207299A1 7946584CB1  
US-10-288-798-44

Query Match 80.0%; Score 1188.2; DB 16; Length 1594;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 402 CCATGGAGCGAACAACCTTCAAGAAAACCAACAGTGTGTGATGAAAATGAAGATGTCAACT 461  
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Db 462 TTGACCACTTTGAAATTTGCGACCATTTGGAAAGGAGTGTGGGAGGTCTGCAATTG 521  
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Db 522 TACAGAAGATGATACCAAGAAGATGTGCGCAATGAAGTACATCAATATAAACAAGTGGC 581  
Qy 181 TGGAGCGCATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGGGTCTGAGC 240  
Db 582 TGGAGCGCATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGGGTCTGAGC 641  
Qy 241 ACCCTTCCCTGGTAAATTTGGTATCTCTTCCAGATGAGGAGACATGTTCAATGCTGG 300  
Db 642 ACCCTTCCCTGGTAAATTTGGTATCTCTTCCAGATGAGGAGACATGTTCAATGCTGG 701  
Qy 301 TGGACCTCTCTGCGGTGGAGACCTGCGGTATATCACTTCCACAGACAGCTTCCACTTCAAG 360

Db 702 TGGACCTCTCTGCGGTGGAGACCTGCGGTATCACTGCAACAGACGTCCACTTCAAGG 761  
Qy 361 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGTGATGCGCCCTGGACTACTGCAAGAAC 420  
Db 762 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGTGATGCGCCCTGGACTACTGCAAGAAC 821  
Qy 421 AGGCGCATCTTCAACAGGATATCAAGCCTGACAAATATTTTACTTGCAGAACATGGGCAG 480  
Db 822 AGGCGCATCTTCAACAGGATATGAGCCTGACAAATATTTTACTTGCAGAACATGGGCAG 881  
Qy 481 TGCACATCAACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTAACACCA 540  
Db 882 TGCACATCAACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTAACACCA 941  
Qy 541 TGGCTGGCAACAGCCTTACATGCGACCTGAGATGTTGAGTCCAGAAAGGAGCAGCT 600  
Db 942 TGGCTGGCAACAGCCTTACATGCGACCTGAGATGTTGAGTCCAGAAAGGAGCAGCT 1001  
Qy 601 ATTCTTTGCTGTTGACTGGTGGTCCCTGGAGTGCAGCGCATATGAATCTCTGAGAGGCC 660  
Db 1002 ATTCTTTGCTGTTGACTGGTGGTCCCTGGAGTGCAGCGCATATGAATCTCTGAGAGGCC 1061  
Qy 661 GAGAGCCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACAGTTTGA 720  
Db 1062 GAGAGCCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACAGTTTGA 1121  
Qy 721 CGACTGTTGTAACCTTACCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 1122 CGACTGTTGTAACCTTACCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181  
Qy 781 TACTCGAACCTTAATCCAGACCAAGATTTTCTCAGTATATCTGATGTCAGAACCTTCCCGT 840  
Db 1182 TACTCGAACCTTAATCCAGACCAAGATTTTCTCAGTATATCTGATGTCAGAACCTTCCCGT 1241  
Qy 841 ATATGAATGATATAAACTGGGATGCGATTTTTCAGAGAGGCTCATTTCCAGGTTTCAATC 900  
Db 1242 ATATGAATGATATAAACTGGGATGCGATTTTTCAGAGAGGCTCATTTCCAGGTTTCAATC 1301  
Qy 901 CTAATAAGCAGCTGAATTTGATGCTTACCTTGTGAACTTTGAGGAATGATTTTGGAGT 960  
Db 1302 CTAATAAGCAGCTGAATTTGATGCTTACCTTGTGAACTTTGAGGAATGATTTTGGAGT 1361  
Qy 961 CCAAACTCTACATAAGAAAAAAGCGCTGCGCAAGAGAGAGATATGAGGAAT 1020  
Db 1362 CCAAACTCTACATAAGAAAAAAGCGCTGCGCAAGAGAGAGATATGAGGAAT 1421  
Qy 1021 GCGATTTCTCTCAGACATGCTTTCTTCAAGAGCACCTTTGACTCTGTCCAGAGAGGATTC 1080  
Db 1422 GCGATTTCTCTCAGACATGCTTTCTTCAAGAGCACCTTTGACTCTGTCCAGAGAGGATTC 1481  
Qy 1081 TAATTTTCAACAGAAAAAGTAAACAGGACCTTTTAAACAAAGACCAACCAATCTAGCCT 1140  
Db 1482 TAATTTTCAACAGAAAAAGTAAACAGGACCTTTTAAACAAAGACCAACCAATCTAGCCT 1541  
Qy 1141 TGGAAACAAACCAAGACCCCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1193  
Db 1542 TGGAAACAAACCAAGACCCCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1594

## RESULT 8

US-09-841-683-10  
Sequence 10, Application US/09841683  
Patent No. US20020081600A1  
GENERAL INFORMATION:  
APPLICANT: Nepomnichy, Boris  
APPLICANT: Hu, Yi  
APPLICANT: Wang, Xiaoming  
APPLICANT: Donoho, Gregory  
APPLICANT: Scoville, John  
APPLICANT: Walke, D. Wade  
TITLE OF INVENTION: No. US20020081600A1 Human Kinase Proteins and Polynucleotides  
FILE REFERENCE: LEX-0167-USA

CURRENT APPLICATION NUMBER: US/09/841,683  
CURRENT FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: US 60/199,499  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: US 60/201,227  
PRIOR FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 1191  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-841-683-10

Query Match 79.9%; Score 1186.2; DB 9; Length 1191;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	3	ATGGGAGCGAACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT	62
DB	1	ATGGGAGCGAACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT	60
QY	63	GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGTCTGCAATTGTA	122
DB	61	GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGTCTGCAATTGTA	120
QY	123	CAGAGATGATACCAAGAGATGTGGCAATGATGATGATGATGATGATGATGATGATGATG	182
DB	121	CAGAGATGATACCAAGAGATGTGGCAATGATGATGATGATGATGATGATGATGATGATG	180
QY	183	GAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGAGGCTCTGGAGCAC	242
DB	181	GAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGAGGCTCTGGAGCAC	240
QY	243	CTTTCTCTGTTAATTTGGTATTCCTTCAAGATGAGAAACATGTTTCATGTTGGTG	302
DB	241	CTTTCTCTGTTAATTTGGTATTCCTTCAAGATGAGAAACATGTTTCATGTTGGTG	300
QY	303	GACCTCTCTGTTGGTGAAGCTGCTGATCCTGCAAGCAAGCAAGCTTCAAGGAA	362
DB	301	GACCTCTCTGTTGGTGAAGCTGCTGATCCTGCAAGCAAGCAAGCTTCAAGGAA	360
QY	363	GAACAGTGAAGCTTCTCATCTGTGAGCTGCTGATGCTGATGCTGATGCTGATGCTG	422
DB	361	GAACAGTGAAGCTTCTCATCTGTGAGCTGCTGATGCTGATGCTGATGCTGATGCTG	420
QY	423	CGCATCATTCAGAGGATATGAGCTGCAAAATATTTTACTTGACGAAATGAGGCGCGT	482
DB	421	CGCATCATTCAGAGGATATGAGCTGCAAAATATTTTACTTGACGAAATGAGGCGCGT	480
QY	483	CACATCACAGATTTCAACATTTGCTGCGATGCTGCGGAGGAGACACAGATTTACCATG	542
DB	481	CACATCACAGATTTCAACATTTGCTGCGATGCTGCGGAGGAGACACAGATTTACCATG	540
QY	543	GCTGGCAACCAAGCTTACATGGCACTGAGATGTTTCAAGTCCAGAAAGGAGGAGGCTAT	602
DB	541	GCTGGCAACCAAGCTTACATGGCACTGAGATGTTTCAAGTCCAGAAAGGAGGAGGCTAT	600
QY	603	TCCTTTGCTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	662
DB	601	TCCTTTGCTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
QY	663	AGACCGTATCATTTCTGCTCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGGAGCG	722
DB	661	AGACCGTATCATTTCTGCTCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGGAGCG	720
QY	723	ACTGTTGAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	782
DB	721	ACTGTTGAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
QY	783	CTGCAACCTAATCAGACCAACAGATTTTCTCAGTTATCTGATGCTCAGACACTTCCCGTAT	842
DB	781	CTGCAACCTAATCAGACCAACAGATTTTCTCAGTTATCTGATGCTCAGACACTTCCCGTAT	840

## RESULT 9

US-10-410-764-102  
; Sequence 102, Application US/10410764  
; Publication No. US200400056641  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Macbeth, Kyle J.  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Rudolph-Owen, Laura A.  
; APPLICANT: Weich, Nadine S.  
; APPLICANT: Olandt, Peter J.  
; APPLICANT: Tsai, Fong-Ying  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Carroll, Joseph M.  
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,  
; TITLE OF INVENTION: 59764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,  
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MPI03-0520NIN  
; CURRENT APPLICATION NUMBER: US/10/410,764  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: US 09/924,358  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/229,300  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: US 10/350,553  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: US 60/351,572  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: US 09/966,614  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/238,054  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: US 10/281,094  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US 60/347,815  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 10/076,535  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/269,440  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 102  
; LENGTH: 1191  
; TYPE: DNA



; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)....(1191)

US-10-410-764-102

Query Match 79.8%; Score 1184.6; DB 16; Length 1191;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1187; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 3 ATGGAGGGAACACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 62
Db 1 ATGGAGGCAACACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 60
Qy 63 GACCACTTTGAAATTTTGGAGCCATTGGGAAGGACGTTTGGGAGGCTTGCATTCTTA 122
Db 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAGGACGTTTGGGAGGCTTGCATTCTTA 120
Qy 123 CAGAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCCTG 182
Db 121 CAGAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGTGCCTG 180
Qy 183 GAGCCAAATGAAGTGAAGAAATGCTTCAAGGAATCTCCAGATCATGACAGGGTCTGGAGCAC 242
Db 181 GAGCCAAATGAAGTGAAGAAATGCTTCAAGGAATCTCCAGATCATGACAGGGTCTGGAGCAC 240
Qy 243 CCTTTCTGTTAAATTTGTGTTATTCCTTCCAGATGAGGAGACATGTTTATGTTGGT 302
Db 241 CCTTTCTGTTAAATTTGTGTTATTCCTTCCAGATGAGGAGACATGTTTATGTTGGT 300
Qy 303 GACCTCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAGCTCCACTTCAAGAA 362
Db 301 GACCTCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAGCTCCACTTCAAGAA 360
Qy 363 GAAACAGTGAAGCTTTCATCTGTGAGTGTGTCATGCGCCCTGGAATCTCTGAGAAC 422
Db 361 GAAACAGTGAAGCTTTCATCTGTGAGTGTGTCATGCGCCCTGGAATCTCTGAGAAC 420
Qy 423 GGCATCATTTACAGGGATATGAAGCTGCACATATTTTACTTGAAGAACATGGGACCTG 482
Db 421 GGCATCATTTACAGGGATATGAAGCTGCACATATTTTACTTGAAGAACATGGGACCTG 480
Qy 483 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTAACACCATG 542
Db 481 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGATACAGATTAACACCATG 540
Qy 543 GCTGCACCAAGCTTACATGACCATGATGTTTCAAGTCTCAGAAAGAGAGAGGCTAT 602
Db 541 GCTGCACCAAGCTTACATGACCATGATGTTTCAAGTCTCAGAAAGAGAGAGGCTAT 600
Qy 603 TCCTTTGCTGTTGACTGGTGTTCCTGGAGTGCAGGATATGAATCTGAGAGGCCGG 662
Db 601 TCCTTTGCTGTTGACTGGTGTTCCTGGAGTGCAGGATATGAATCTGAGAGGCCGG 660
Qy 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTTCAGAG 722
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTTCAGAG 720
Qy 723 ACTGTTGTAACCTTACCTTCCCTGCTGCTGCTCAGGAAATGCTGCTCTTAAAGCTA 782
Db 721 ACTGTTGTAACCTTACCTTCCCTGCTGCTGCTCAGGAAATGCTGCTCTTAAAGCTA 780
Qy 783 CTCGAACCTTAATCCAGAACCAAGTATTTCTCAGTTTATCTGATGTCAGAACTTCCCGTAT 842
Db 781 CTCGAACCTTAATCCAGAACCAAGTATTTCTCAGTTTATCTGATGTCAGAACTTCCCGTAT 840
Qy 843 ATGAATGATATAAATCTGGGATGAGTGTTCAGAAAGAGGCTCATTTCCAGGTTTCAATCCT 902
Db 841 ATGAATGATATAAATCTGGGATGAGTGTTCAGAAAGAGGCTCATTTCCAGGTTTCAATCCT 900
Qy 903 AATAAGGAGGCTGAAATTTGTGATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 962
Db 901 AATAAGGAGGCTGAAATTTGTGATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 960
```

## RESULT 10

US-09-841-683-12

; Sequence 12, Application US/09841683

; Patent No. US2002081600A1

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. US2002081600A1el Human Kinase Proteins and Polynucleotides

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 1675

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-841-683-12

Query Match 78.3%; Score 1162.6; DB 9; Length 1675;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy 1 CCATGGGAGCGAACACACTTCAAGAAAAACCAACAGATGTTTGTGATGAAAAATGAAGATGTCAACT 60
Db 411 CCATGGGAGCGAACACACTTCAAGAAAAACCAACAGATGTTTGTGATGAAAAATGAAGATGTCAACT 470
Qy 61 TTGACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGACGTTTGGGGAGGTCTGCATTG 120
Db 471 TTGACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGACGTTTGGGGAGGTCTGCATTG 530
Qy 121 TACAGAGAAATGATACCAAGAGATGTCCGCAATGAGTACATGAATAAACAAGATGCG 180
Db 531 TACAGAGAAATGATACCAAGAGATGTCCGCAATGAGTACATGAATAAACAAGATGCG 590
Qy 181 TGGAGCGCAATGAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGACGGGTCTGGAGC 240
Db 591 TGGAGCGCAATGAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGACGGGTCTGGAGC 650
Qy 241 ACCCTTCTCGGTTAAATTTGTGTTATTCCTTTCCAAAGATGAGGAAAGACATGTTCATGTTGG 300
Db 651 ACCCTTCTCGGTTAAATTTGTGTTATTCCTTTCCAAAGATGAGGAAAGACATGTTCATGTTGG 710
Qy 301 TGGACCTCTCTGGGTGGAGACCTGGTTATCACCTGCAACAGAACGTCCTCACTTCAAGG 360
Db 711 TGGACCTCTCTGGGTGGAGACCTGGTTATCACCTGCAACAGAACGTCCTCACTTCAAGG 770
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361	QY	AAGAAACAGTGAAGACTTTCATCTGTGAGCTGTGTATGGCCCTGGACTACCTGCGAAGCC	420
771	DB	AAGAAACAGTGAAGCTTTCATCTGTGAGCTGTGTATGGCCCTGGACTACCTGCGAAGCC	830
421	QY	AGCGCATCATTTACAGGGATATGAAGCCTGACAAATATTTTACTTTGACGAACATGGGCACG	480
831	DB	AGCGCATCATTTACAGGGATATGAAGCCTGACAAATATTTTACTTTGACGAACATGGGCACG	890
481	QY	TGCACATTCACAGATTTTCAACATTTGCTGCGATGTGCCCAGGGAGACACAGATTTACACCA	540
891	DB	TGCACATTCACAGATTTTCAACATTTGCTGCGATGTGCCCAGGGAGACACAGATTTACACCA	950
541	QY	TGCTGCGACCAAGCCCTTACATGGCACCTCAGAGATGTTTCAGCTCCAGAAAGGAGCAGGCT	600
951	DB	TGCTGCGACCAAGCCCTTACATGGCACCTCAGAGATGTTTCAGCTCCAGAAAGGAGCAGGCT	1010
601	QY	ATTCCCTTTGCTGTTGACTGTGTGCTCCGTGGGAGTGACGGCATATGAATCTGCTCAGAGGCC	660
1011	DB	ATTCCCTTTGCTGTTGACTGTGTGCTCCGTGGGAGTGACGGCATATGAATCTGCTCAGAGGCC	1070
661	QY	GGAGACCGTATCATATTTGCGTCCAGTACTTTCACAGCAAGGAAATTTGTACACACGTTTGAGA	720
1071	DB	GGAGACCGTATCATATTTGCGTCCAGTACTTTCACAGCAAGGAAATTTGTACACACGTTTGAGA	1130
721	QY	CGACTGTTGTAACTTACCCCTTCGCTGCTGTCACAGGAAATGCGTCACTTCTTAAAGGC	780
1131	DB	CGACTGTTGTAACTTACCCCTTCGCTGCTGTCACAGGAAATGCGTCACTTCTTAAAGGC	1190
781	QY	TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTTATCTGATGTCCAGAACTTCCCGT	840
1191	DB	TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTTATCTGATGTCCAGAACTTCCCGT	1250
841	QY	ATATGAATGATATAAATCTGGGATGCAAGTTTTTTCAGAAAGCGCTCATTTCCAGGTTTCATTC	900
1251	DB	ATATGAATGATATAAATCTGGGATGCAAGTTTTTTCAGAAAGCGCTCATTTCCAGGTTTCATTC	1310
901	QY	CTAATAAGGCGCGCTGAAATTTGTGATCCTACCTTTTGAACTTTGAGGAAATGATTTTCGAGT	960
1311	DB	CTAATAAGGCGCGCTGAAATTTGTGATCCTACCTTTTGAACTTTGAGGAAATGATTTTCGAGT	1370
961	QY	CCAAACCTCTACATAGAAGAAAAAGCGTCTGGCAAGAGAGGAGGATATCAGGAAAT	1020
1371	DB	CCAAACCTCTACATAGAAGAAAAAGCGTCTGGCAAGAGAGGAGGATATCAGGAAAT	1430
1021	QY	CGGATTTCTTCAGACATGCTTCTTTCAGAGCACCCTTGACTCTGTCCAGAGAGGATTCA	1080
1431	DB	CGGATTTCTTCAGACATGCTTCTTTCAGAGCACCCTTGACTCTGTCCAGAGAGGATTCA	1490
1081	QY	TAATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAGACCAACCAATCTAGCCT	1140
1491	DB	TAATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAGACCAACCAATCTAGCCT	1550
1141	QY	TGGAAACAAACCAAGAGCCCAAGGGTGAGGATGGTCTCAGATAACA	1185
1551	DB	TGGAAACAAACCAAGAGCCCAAGGTGACAAATGGACAAATGGACAA	1595

RESULT 11

US-09-841-683-8

US 05 041 003-8  
; Sequence 8, Application US/09841683

; Sequence 6, Application US  
; Patent No. US20020081600A1

; FACEID NO: 032002008;  
; GENERAL INFORMATION:

: APPLICANT: HU. YI

APPLICANT: Nepomnichy, Boris

APPLICANT: Wang, Xiaoming

APPLICANT: Wang, Xiaoming

APPLICANT: Donoho, Gregory

APPLICANT: Donoho, Gregory  
APPLICANT: Scoville, John

APPLICANT: Scoville, John  
APPLICANT: Walke D Wade

APPLICANT: WALKER, D. WADDE  
TITLE OF INVENTION: NO. 1152003

; TITLE OF INVENTION: No. US2002  
 ; FILE REFERENCE: LEX-0167-JUSA

FILE REFERENCE: LEX-0167-USA  
CURRENT APPLICATION NUMBER: IIS/08/841 683

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; CURRENT APPLICATION NUMBER: US/09
: CURRENT FILING DATE: 2001 04 24

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; CURRENT FILING DATE: 2001-04-24  
 ; PRIOR APPLICATION NUMBER: US 60/100 400

Db 841 ATGAATGATATAAACTGGATGCGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCT 900  
Qy 903 AATAAGGCGAGCTGAATGTGATCTTACCTTTGAACTTGAGGAAATGATTTGGAGTCC 962  
Db 901 AATAAGGCGAGCTGAATGTGATCTTACCTTTGAACTTGAGGAAATGATTTGGAGTCC 960  
Qy 963 AAACCTCTACATAGAGAAAAAGCGCTGCGAAAGAGGAGGAGATATCAGGAAATGC 1022  
Db 961 AAACCTCTACATAGAGAAAAAGCGCTGCGAAAGAGGAGGAGATATGAGGAAATGC 1020  
Qy 1023 GATTCTTCTCAGACATGTCCTTCTTCAAGAGCACCTTGATCTCTGTCAGAGGAGTTTCATA 1082  
Db 1021 GATTCTTCTCAGACATGTCCTTCTTCAAGAGCACCTTGATCTCTGTCAGAGGAGTTTCATA 1080  
Qy 1083 ATTTTCAAGAGAAAAAGTAAACAGGACCTTTAAACAAAGACCAACCAAAATCTAGCCTTG 1142  
Db 1081 ATTTTCAAGAGAAAAAGTAAACAGGACCTTTAAACAAAGACCAACCAAAATCTAGCCTTG 1140  
Qy 1143 GAACAAACCAAGAGCCCAAGGTGAGGATGCTCAGAATAACA 1185  
Db 1141 GAACAAACCAAGAGCCCAAGGTGAGGATGCTCAGAATAACA 1183

## RESULT 12

US-10-108-260A-231

; Sequence 231, Application US/10108260A

; Publication No. US20040005560A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA

; FILE REFERENCE: H1-A0106

; CURRENT APPLICATION NUMBER: US/10/108,260A

; CURRENT FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 5458

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 231

; LENGTH: 2063

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-108-260A-231

Query Match 69.3%; Score 1029.4; DB 16; Length 2063;  
Best Local Similarity 99.4%; Pred. No. 2.2e-300;  
Matches 1033; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCATGGGAGCGAACACTTCAAGAAACCAACGATGTTTGTGATGAAATGAAGATGTCAACT 60  
Db 332 CCATGGGAGCGAACACTTCAAGAAACCAACGATGTTTGTGATGAAATGAAGATGTCAACT 391  
Qy 61 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGCTCTGCATTG 120  
Db 392 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGCTCTGCATTG 451  
Qy 121 TACAGAAGATGATACCAAGAGATGTGGCAATGAAGTACATGAATAAACAAAAGTGGC 180  
Db 452 TACAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAAAGTGGC 511  
Qy 181 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGAGGCTCTGGAGC 240  
Db 512 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGAGGCTCTGGAGC 571  
Qy 241 ACCCTTCTCTGTTAAATTTGTGTTATCTTCCAAAGATGAGGAGACATGTTTCATGTTGG 300  
Db 572 ACCCTTCTCTGTTAAATTTGTGTTATCTTCCAAAGATGAGGAGACATGTTTCATGTTGG 631  
Qy 301 TGGACCTCTCTGTTGGTGGAGACCTCGCGTTATCCTTCACATGCAACAGAACGTCCACTTCAAGG 360  
Db 632 TGGACCTCTCTGTTGGTGGAGACCTCGCGTTATCCTTCACATGCAACAGAACGTCCACTTCAAGG 691  
Qy 361 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGTATGCGCCCTGGAACCTACCTGCAAGAAC 420  
Db 692 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGTATGCGCCCTGGAACCTACCTGCAAGAAC 751

Qy 421 AGCGCATCATTTACAGGAGATATGAAGCCTGCACATATATTTTACTTGCAGAACATGGGCAGC 480  
Db 752 AGCGCATCATTTACAGGAGATATGAAGCCTGCACATATATTTTACTTGCAGAACATGGGCAGC 811  
Qy 481 TGCACATCAGAGATTTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTAACCA 540  
Db 812 TGCACATCAGAGATTTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTAACCA 871  
Qy 541 TGGCTGCGACCAAGCCTTACATGCGCACCTGAGATGTTTCAAGTCCAGAAAAGGAGCAGGCT 600  
Db 872 TGGCTGCGACCAAGCCTTACATGCGCACCTGAGATGTTTCAAGTCCAGAAAAGGAGCAGGCT 931  
Qy 601 ATTCCTTTTGTGTTGACTGCTGGAGTGGTCCCTGGAGTGACGGCATATGAATCTGCTGAGAGGCC 660  
Db 932 ATTCCTTTTGTGTTGACTGCTGGAGTGGTCCCTGGAGTGACGGCATATGAATCTGCTGAGAGGCC 991  
Qy 661 GGAGACCGTATCATATTTGCTTCCAGTACTTCCAGCAAGGAAATTTGTACACAGTTTGAGA 720  
Db 992 GGAGACCGTATCATATTTGCTTCCAGTACTTCCAGCAAGGAAATTTGTACACAGTTTGAGA 1051  
Qy 721 CGACTGTTGTAACCTTACCCTTCTGCTGGTGCACAGGAAATGGTGTCTACTTCTTAAAAAGC 780  
Db 1052 CGACTGTTGTAACCTTACCCTTCTGCTGGTGCACAGGAAATGGTGTCTACTTCTTAAAAAGC 1111  
Qy 781 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840  
Db 1112 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 1171  
Qy 841 ATATGAATGATATAAACTGGGATGCGAGTCTTTTTCAGAAAGAGGCTCATTTCCAGGTTTCAATC 900  
Db 1172 ATATGAATGATATAAACTGGGATGCGAGTCTTTTTCAGAAAGAGGCTCATTTCCAGGTTTCAATC 1231  
Qy 901 CTAATAAGGCGAGCTGAATTTGTGATCCTTACCTTTGAACTTTGAGAAATGATTTTGGAGT 960  
Db 1232 CTAATAAGGCGAGCTGAATTTGTGATCCTTACCTTTGAACTTTGAGAAATGATTTTGGAGT 1291  
Qy 961 CCAAACTCTACATAAGAAAAAAGCGCTCTGCAAGAGAGGAGGAGGATATGAGGAAAT 1020  
Db 1292 CCAAACTCTACATAAGAAAAAAGCGCTCTGCAAGAGAGGAGGAGGATATGAGGAAAT 1351  
Qy 1021 GCGATTCTTCTCAGACATG 1039  
Db 1352 GCGATTCTTCTCAGGTAAG 1370

## RESULT 13

US-10-276-774-239

; Sequence 239, Application US/10276774

; Publication No. US20040053245A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

; FILE REFERENCE: 21272-030

; CURRENT APPLICATION NUMBER: US/10/276,774

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 09/560,875

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 09/496,914

; PRIOR FILING DATE: 2000-02-03

; NUMBER OF SEQ ID NOS: 2700

; SOFTWARE: Custom

; SEQ ID NO 239

; LENGTH: 678

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-276-774-239

Query Match 45.3%; Score 672.8; DB 13; Length 678;  
Best Local Similarity 99.7%; Pred. No. 1.2e-192;  
Matches 674; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 441 ATGAAGCCTGACAAATATTTTACTTGCAGAACATGGGCGCTGCACATCAACAGATTTTCAAC 500

Db 1 ATGAAGCCTGACAAATATTTTACTTGACGAACATGGGCACGTGCACATCACAGATTTCAAC 60  
Qy 501 ATTGCTCGATGTGCTCCAGGAGACACAGATTACCAACCATGCTGCGCACCAGCCTTAC 560  
Db 61 ATTGCTCGATGTGCTCCAGGAGACACAGATTACCAACCATGCTGCGCACCAGCCTTAC 120  
Qy 561 ATGGCAGCTGAGATGTTTCACTCCAGAAAGAGAGAGGCTATTTCCTTTGCTGTTGACTGG 620  
Db 121 ATGGCAGCTGAGATGTTTCACTCCAGAAAGAGAGAGGCTATTTCCTTTGCTGTTGACTGG 180  
Qy 621 TGGTCCCTGGAGTGACGCGCATATGAATGCTGAGAGGCGGAGAGCGGTATCATATATTCGC 680  
Db 181 TGGTCCCTGGAGTGACGCGCATATGAATGCTGAGAGGCGGAGAGCGGTATCATATATTCGC 240  
Qy 681 TCCAGTACTTCCAGCAAGGAAATGTTATACACAGTTTGAACGAGCTGTTGTAATTCACCT 740  
Db 241 TCCAGTACTTCCAGCAAGGAAATGTTATACACAGTTTGAACGAGCTGTTGTAATTCACCT 300  
Qy 741 TCTGCTGCTGACAGGAAATGTTGTCACCTTCTTAAAGGCTCTCGAACCTTATCCAGAC 800  
Db 301 TCTGCTGCTGACAGGAAATGTTGTCACCTTCTTAAAGGCTCTCGAACCTTATCCAGAC 360  
Qy 801 CAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTATATGATGATATATAAATCGG 860  
Db 361 CAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTATATGATGATATATAAATCGG 420  
Qy 861 GATGCAATTTTCCAGAGAGGCTCATTTCCAGTTTCACTTCTTAAAGGCTCTCGAACCTTAT 920  
Db 421 GATGCAATTTTCCAGAGAGGCTCATTTCCAGTTTCACTTCTTAAAGGCTCTCGAACCTTAT 480  
Qy 921 TGTGATCCTACCTTTGAACTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAGAAA 980  
Db 481 TGTGATCCTACCTTTGAACTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAGAAA 540  
Qy 981 AAAAAGCTCTGGCAAGAGGAGGATATGAGGAATGCGAATCTTCTTCAGACATGT 1040  
Db 541 AAAAAGCTCTGGCAAGAGGAGGATATGAGGAATGCGAATCTTCTTCAGACATGT 600  
Qy 1041 CTTCTCAGAGCACTTGACTGTCAGAGAGGATTCATATTTTCAACAGAGAAAA 1100  
Db 601 CTTCTCAGAGCACTTGACTGTCAGAGAGGATTCATATTTTCAACAGAGAAAA 660  
Qy 1101 GTAAACAGGACTTTA 1116  
Db 661 GTAAACAGGACTGTA 676

## RESULT 14

US-09-841-683-6

; Sequence 6, Application US/09841683

; Patent No. US20020081600A1

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; PRIOR FILING DATE: 2001-04-24

; PRIOR FILING DATE: 2000-04-25

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 711

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-841-683-6

Query Match 44.2%; Score 656.2; DB 9; Length 711;

Best Local Similarity 99.5%; Pred. No. 1.3e-187;

Matches 658; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGGAGCGAACAACCTTCAAGAAACCCAGGTTTGTATGAATAATGAAGATGTCAACTTT 62  
Db 1 ATGGGAGCGAACAACCTTCAAGAAACCCAGGTTTGTATGAATAATGAAGATGTCAACTTT 60  
Qy 63 GACCACTTTGAAATTTTGGAGCCCATTTGGAAAGGAGGTTTGGGAGGTTTGGGAGGTTT 122  
Db 61 GACCACTTTGAAATTTTGGAGCCCATTTGGAAAGGAGGTTTGGGAGGTTTGGGAGGTTT 120  
Qy 123 CAGAGATATGATACCAAGAGATGTCGCAATGAAGTACATGATTAACAAAAGTGGCTG 182  
Db 121 CAGAGATATGATACCAAGAGATGTCGCAATGAAGTACATGATTAACAAAAGTGGCTG 180  
Qy 183 GAGCGCAATGAAGTGAAGAAATGTTCTTCAAGGAACTTCCAGATCATGTCAGGGTCTGAGAC 242  
Db 181 GAGCGCAATGAAGTGAAGAAATGTTCTTCAAGGAACTTCCAGATCATGTCAGGGTCTGAGAC 240  
Qy 243 CTTTCTCTGTTAAATTTGTTGTTATTCCTTCCAGATGAGGAAGATGTTCTATGTTGTTG 302  
Db 241 CTTTCTCTGTTAAATTTGTTGTTATTCCTTCCAGATGAGGAAGATGTTCTATGTTGTTG 300  
Qy 303 GACCTCTCTGTTGAGACCTGCTTATCACCTGCAACAGAACGTTCCACTTCAAGGAA 362  
Db 301 GACCTCTCTGTTGAGACCTGCTTATCACCTGCAACAGAACGTTCCACTTCAAGGAA 360  
Qy 363 GAAACAGTCAAGCTCTTTCATCTGTGAGCTGTCATGCGCCCTGCACTTACCTGCAAGACCAG 422  
Db 361 GAAACAGTCAAGCTCTTTCATCTGTGAGCTGTCATGCGCCCTGCACTTACCTGCAAGACCAG 420  
Qy 423 CGCATCATTTCAAGGATATGAAGCTGCAATATTTTATCTTGAACGAAATGAGGACGCTG 482  
Db 421 CGCATCATTTCAAGGATATGAAGCTGCAATATTTTATCTTGAACGAAATGAGGACGCTG 480  
Qy 483 CACATCACAGATTTCAACATTCCTGCGATGTCGCCAGGAGACACAGATTTACCACTATG 542  
Db 481 CACATCACAGATTTCAACATTCCTGCGATGTCGCCAGGAGACACAGATTTACCACTATG 540  
Qy 543 GCTGGCAACCAAGCTTTACATGTCACCTGAGATGTTTCAGCTCCAGAAAGGAGAGGAGCTAT 602  
Db 541 GCTGGCAACCAAGCTTTACATGTCACCTGAGATGTTTCAGCTCCAGAAAGGAGAGGAGCTAT 600  
Qy 603 TCCTTTGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662  
Db 601 TCCTTTGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Qy 663 A 663  
Db 661 A 661

## RESULT 15

US-09-841-683-4

; Sequence 4, Application US/09841683

; Patent No. US20020081600A1

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 678  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-841-683-4

Query Match 44.1%; Score 655.2; DB 9; Length 678;  
Best Local Similarity 99.5%; Pred. No. 2.6e-187;  
Matches 657; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db	1	ATGGGAGCGACACCTTCAAGAAACACCACCACTGTTGATGAATGAAGATGTCACCTTT	60
Qy	63	GACCACCTTTGAAATTTTGGAGGCCATTTGGGAAAGCGAGTTTGGGAGGCTCTGCATTGTA	122
Db	61	GACCACCTTTGAAATTTTGGAGGCCATTTGGGAAAGCGAGTTTGGGAGGCTCTGCATTGTA	120
Qy	123	CAGAAGATGATACCAAGAAAGATGTGGCAATGAAGTACATGAATAACAAAGTGGGTG	182
Db	121	CAGAAGATGATACCAAGAAAGATGTGGCAATGAAGTACATGAATAACAAAGTGGGTG	180
Qy	183	GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATCGAGGCTCTGGAGCAC	242
Db	181	GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATCGAGGCTCTGGAGCAC	240
Qy	243	CCTTTCCTGGTTAAATTTGTGGTATTCTTCAAGATGAGGAAGACATGTTTCATGTTGGTG	302
Db	241	CCTTTCCTGGTTAAATTTGTGGTATTCTTCAAGATGAGGAAGACATGTTTCATGTTGGTG	300
Qy	303	GACCTCTGCTGGGTGGAGACCTGGGTTATCACTGCAACAGAACTCCACTTCAAGGAA	362
Db	301	GACCTCTGCTGGGTGGAGACCTGGGTTATCACTGCAACAGAACTCCACTTCAAGGAA	360
Qy	363	GAAACAGTGAAGCTCTTCATCTGTGAGCTGTGCTCATGGCCCTGGACTACCTGCAGAACG	422
Db	361	GAAACAGTGAAGCTCTTCATCTGTGAGCTGTGCTCATGGCCCTGGACTACCTGCAGAACG	420
Qy	423	CGCATCATTCACAGGGATATGAAGCTGACAAATATTTTACCTTGACGAACATGGGCACTG	482
Db	421	CGCATCATTCACAGGGATATGAAGCTGACAAATATTTTACCTTGACGAACATGGGCACTG	480
Qy	483	CACATCAGATTTCAACATTTGCTGGATGCTGCCAGGGAGACACAGATTACCACCATG	542
Db	481	CACATCAGATTTCAACATTTGCTGGATGCTGCCAGGGAGACACAGATTACCACCATG	540
Qy	543	GCTGGCACCAGCCTTACATGGCACCTGAGATGTTCACTCCAGAAAGGAGCAGGCTAT	602
Db	541	GCTGGCACCAGCCTTACATGGCACCTGAGATGTTCACTCCAGAAAGGAGCAGGCTAT	600
Qy	603	TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGAAGGAGTGAATGCTGAGAGGCCGG	662
Db	601	TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGAAGGAGTGAATGCTGAGAGGCCGG	660

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Job time : 504 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-10-667-442-1

Perfect score: 1485

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Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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  - 2: /cgn2\_6/ptodata/2/ina/5B COMB.seq:\*
  - 3: /cgn2\_6/ptodata/2/ina/6A COMB.seq:\*
  - 4: /cgn2\_6/ptodata/2/ina/6B COMB.seq:\*
  - 5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq:\*
  - 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1485	100.0	1485	4	US-09-801-876B-1
2	1485	100.0	1485	4	US-10-254-869-1
3	1186.2	79.9	1191	4	US-09-841-683-10
4	1182.6	78.3	1675	4	US-09-841-683-12
5	1180.6	78.2	1224	4	US-09-841-683-8
6	656.2	44.2	711	4	US-09-841-683-6
7	655.2	44.1	678	4	US-09-841-683-4
8	481.6	32.4	1257	4	US-09-799-875-15
9	481.6	32.4	1826	4	US-09-799-875-13
10	466.8	31.4	1864	4	US-09-819-607-1
11	363.4	24.5	148567	4	US-09-801-876B-3
12	363.4	24.5	148567	4	US-10-254-869-3
13	132.6	8.9	1008	4	US-09-394-455-3
14	132.6	8.9	2549	3	US-09-467-082-3
15	132.6	8.9	2549	4	US-09-394-455-5
16	132.6	8.9	2608	4	US-09-394-455-35
17	132	8.9	1619	4	US-09-394-455-14
18	132.6	8.3	25603	4	US-09-819-607-3
19	120.4	8.1	1498	4	US-09-509-902A-6
20	120.4	8.1	1961	4	US-09-509-902A-15
21	120.4	8.1	2204	1	US-08-221-817-12
22	120.4	8.1	2204	1	US-08-454-439-12
23	120.4	8.1	2204	5	PCT-US94-10487-10
24	120.4	8.1	2206	1	US-08-221-817-10
25	120.4	8.1	2206	1	US-08-454-439-10
26	120.4	8.1	2206	5	PCT-US94-10487-10
27	120.4	8.1	2848	3	US-08-464-954A-2

28 120.4 8.1 5276 4 US-09-233-857-2 Sequence 2, Appli  
29 119.8 8.1 1788 4 US-09-417-197-68 Sequence 68, Appl  
30 119.8 8.1 2211 4 US-09-394-455-39 Sequence 39, Appl  
31 110.8 7.5 1662 4 US-09-802-117-1 Sequence 1, Appli  
32 110.8 7.5 2249 4 US-09-802-117-5 Sequence 5, Appli  
33 109.8 7.4 1599 3 US-09-256-465-1 Sequence 1, Appli  
34 109.8 7.4 1599 4 US-09-167-322-3 Sequence 3, Appli  
35 109.8 7.4 1599 4 US-09-023-655-1004 Sequence 1004, Ap  
36 109.2 7.4 1662 4 US-09-738-894A-1 Sequence 1, Appli  
37 109.2 7.4 1662 4 US-09-964-469-1 Sequence 1, Appli  
38 107.2 7.2 2754 3 US-09-429-322-3 Sequence 3, Appli  
39 106.8 7.2 2370 4 US-09-031-295-1 Sequence 1, Appli  
40 106.8 7.2 4438 4 US-09-566-921-81 Sequence 81, Appl  
41 106.6 7.2 2599 6 5266464-1 Patent No. 5266464  
42 104.6 7.1 2511 4 US-09-417-197-60 Sequence 60, Appl  
43 104.8 7.1 2529 4 US-09-417-197-42 Sequence 42, Appl  
44 104.8 7.1 2557 4 US-09-016-434-1298 Sequence 1298, Ap  
45 104.6 7.0 2057 4 US-09-016-434-1306 Sequence 1306, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-801-876B-1  
; Sequence 1, Application US/09801876B  
; Patent No. 6492155  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: C0001160  
; CURRENT APPLICATION NUMBER: US/09/801,876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1485  
; TYPE: DNA  
; ORGANISM: Human  
US-09-801-876B-1

Query Match 100.0%; Score 1485; DB 4; Length 1485;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGGGAGCGAACAACCTTCAAGAAACCAACCACTGTTGATGAAATGAAGATGTCAACT 60  
Db 1 CCATGGGAGCGAACAACCTTCAAGAAACCAACCACTGTTGATGAAATGAAGATGTCAACT 60

Qy 61 TTGACCACTTTGAAATTTTGGCGAGCCATTGGGAAAGCGAGTTTGGGAGGCTTGCATTG 120  
Db 61 TTGACCACTTTGAAATTTTGGCGAGCCATTGGGAAAGCGAGTTTGGGAGGCTTGCATTG 120

Qy 121 TACAGAGATGATACCAAGAACATGCGCAATGAAGTACATGAATACAAACAAAGTGGC 180  
Db 121 TACAGAGATGATACCAAGAACATGCGCAATGAAGTACATGAATACAAACAAAGTGGC 180

Qy 181 TCGAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGGGTCTGGAGC 240  
Db 181 TCGAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGGGTCTGGAGC 240

Qy 241 ACCCTTTCCTGGTTAATTTGGTGTATTCCTTCAAGATGAAGAGACATGTTCAATGTTGG 300  
Db 241 ACCCTTTCCTGGTTAATTTGGTGTATTCCTTCAAGATGAAGAGACATGTTCAATGTTGG 300

Qy 301 TCGACCTCCCTGGGTGGAGACCTGGTTATCACCTGCAACAGAGCTCCACTTCAAGG 360  
Db 301 TCGACCTCCCTGGGTGGAGACCTGGTTATCACCTGCAACAGAGCTCCACTTCAAGG 360

Qy 361 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGCTGATGGCCCTGGACTACCTGCAAGC 420

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Db 361 AAGAACAGTGAAGCTCTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGCGAACC 420
Qy 421 AGCGCATCTTCAAGGGATATGAAGCCTGACAAATATTTTACTTGAAGCAATGGCGACG 480
Db 421 AGCGCATCTTCAAGGGATATGAAGCCTGACAAATATTTTACTTGAAGCAATGGCGACG 480
Qy 481 TGCACATCAGATTTCAACATTTGCGATCTGCGATCTGCCAGGAGACACAGATTACCA 540
Db 481 TGCACATCAGATTTCAACATTTGCGATCTGCGATCTGCCAGGAGACACAGATTACCA 540
Qy 541 TGGCTGGACCAAGCCTTACATGGCACTTGAAGTGTTCAGTCTCCAGAAAGAGCAGGCT 600
Db 541 TGGCTGGACCAAGCCTTACATGGCACTTGAAGTGTTCAGTCTCCAGAAAGAGCAGGCT 600
Qy 601 ATTCTTTGCTGTGTGATCTGGTGTCTCCAGGAGTGAAGCATATGAATCTGTGAGAGCC 660
Db 601 ATTCTTTGCTGTGTGATCTGGTGTCTCCAGGAGTGAAGCATATGAATCTGTGAGAGCC 660
Qy 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGA 720
Db 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGA 720
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Db 721 CGACTGTGTAACTTACCTTCTGCTGTGTCAAGGAATGGTGTCACTTCTTAAAAAGC 780
Qy 781 TACTGAACTTAATCAGACCAAGATTTTCTCAGTTATCTGATTCAGAACTTCCCGT 840
Db 781 TACTGAACTTAATCAGACCAAGATTTTCTCAGTTATCTGATTCAGAACTTCCCGT 840
Qy 841 ATATGAATCATATAAATCTGGATGTCAGTTTTCAGAAAGGCTTCATTCAGGTTTCATTC 900
Db 841 ATATGAATCATATAAATCTGGATGTCAGTTTTCAGAAAGGCTTCATTCAGGTTTCATTC 900
Qy 901 CTAATAAAGCGAGGCTGAATTTGTGATCTTACCTTTGAACTTGAGGAATGATTTTGGAGT 960
Db 901 CTAATAAAGCGAGGCTGAATTTGTGATCTTACCTTTGAACTTGAGGAATGATTTTGGAGT 960
Qy 961 CCMAACTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAT 1020
Db 961 CCMAACTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAT 1020
Qy 1021 GCGATTTCTTCAGACATGCTTCTTCAAGAGCCTTCACTCTGCTGCCAGAGGAGTTCA 1080
Db 1021 GCGATTTCTTCAGACATGCTTCTTCAAGAGCCTTCACTCTGCTGCCAGAGGAGTTCA 1080
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Db 1081 TAAATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACAACTTAGCCT 1140
Qy 1141 TGGCAACAAACCAAGACCCACAGGTGAGGATGGTCAAGATTAACAATTTGTAAGCCCTC 1200
Db 1141 TGGCAACAAACCAAGACCCACAGGTGAGGATGGTCAAGATTAACAATTTGTAAGCCCTC 1200
Qy 1201 ATGCTCTTCTTGGGACATCTCATGCGACAACTTCTAAATACATATGTCAAGAAAG 1260
Db 1201 ATGCTCTTCTTGGGACATCTCATGCGACAACTTCTAAATACATATGTCAAGAAAG 1260
Qy 1261 CTGACAGTAGCTCTCTGCCACTCCACACACATGACTTAGAAAAATGTGAATGAATATATTT 1320
Db 1261 CTGACAGTAGCTCTCTGCCACTCCACACACATGACTTAGAAAAATGTGAATGAATATATTT 1320
Qy 1321 CAAAAAGGAGCAGACACACAGTGAAGGGTCTGGGCGCTGAGCTCTGGAAAGTCAATTC 1380
Db 1321 CAAAAAGGAGCAGACACACAGTGAAGGGTCTGGGCGCTGAGCTCTGGAAAGTCAATTC 1380
Qy 1381 ACATCAATCAACTGTGTGATCTAGAGCAAGTCACTTAGCCACTTTCTGTGCTTTACTTTA 1440
Db 1381 ACATCAATCAACTGTGTGATCTAGAGCAAGTCACTTAGCCACTTTCTGTGCTTTACTTTA 1440
Qy 1441 TTTATCTAAATGAGAGGGTTATCTTAAAAAAGGAAAAA 1485
Db 1441 TTTATCTAAATGAGAGGGTTATCTTAAAAAAGGAAAAA 1485
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## RESULT 2

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US-10-254-869-1
; Sequence 1, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-10-254-869-1
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Query Match 100.0%; Score 1485; DB 4; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGGGAGCGAACACTTCAAGAAAAACCAACAGTGTGTGTGATGAAAAATGAAGATGCAACT 60
Db 1 CCATGGGAGCGAACACTTCAAGAAAAACCAACAGTGTGTGTGATGAAAAATGAAGATGCAACT 60
Qy 61 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGAGGATTTGGGGAGGTCTGCAATG 120
Db 61 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGAGGATTTGGGGAGGTCTGCAATG 120
Qy 121 TACAGAAAGATGATACCAAGAAAGATGTGCGCAATGAAGTATCATGAATAAACAAAGTGGC 180
Db 121 TACAGAAAGATGATACCAAGAAAGATGTGCGCAATGAAGTATCATGAATAAACAAAGTGGC 180
Qy 181 TGGAGCGCAATGAAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGCAAGGCTCTGGAGC 240
Db 181 TGGAGCGCAATGAAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGCAAGGCTCTGGAGC 240
Qy 241 ACCCTTTCTCTGGTAAATTTGTTGGTATTCCTTCCAAGATGAGGAAAGACATGTTTCATGTTGG 300
Db 241 ACCCTTTCTCTGGTAAATTTGTTGGTATTCCTTCCAAGATGAGGAAAGACATGTTTCATGTTGG 300
Qy 301 TGGACCTCTCTGCTGGGTGGAGACCTGCTTATACCTGCAACAGAAACGTCTCACTTCAAGG 360
Db 301 TGGACCTCTCTGCTGGGTGGAGACCTGCTTATACCTGCAACAGAAACGTCTCACTTCAAGG 360
Qy 361 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGCTGAGTACCTGCAAGAACCC 420
Db 361 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGCTGAGTACCTGCAAGAACCC 420
Qy 421 AGCGCATCATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGAAGCAATGGGACG 480
Db 421 AGCGCATCATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGAAGCAATGGGACG 480
Qy 481 TGCACATCAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTACCA 540
Db 481 TGCACATCAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTACCA 540
Qy 541 TGGCTGGACCAAGCCTTACATGGCACTTGAAGTGTTCAGTCTCCAGAAAGAGCAGGCT 600
Db 541 TGGCTGGACCAAGCCTTACATGGCACTTGAAGTGTTCAGTCTCCAGAAAGAGCAGGCT 600
Qy 601 ATTCTTTGCTGTGTGATCTGGTGTCTCCAGGAGTGAAGCATATGAATCTGTGAGAGGCC 660
Db 601 ATTCTTTGCTGTGTGATCTGGTGTCTCCAGGAGTGAAGCATATGAATCTGTGAGAGGCC 660
Qy 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGA 720
Db 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGA 720
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Db 901 AATAAGGAGGCTGAATTTGATCCTTACCTTTGAACTTGGAGAAATGATTTGGAGTCC 960  
Qy 963 AAACCTCTACATAAGAAAAAAGCGCTCTGGCAAGAGAGAGAGATATGAGAAATGC 1022  
Db 961 AAACCTCTACATAAGAAAAAAGCGCTCTGGCAAGAGAGAGAGATATGAGAAATGC 1020  
Qy 1023 GATTTCTCTCAGACATGTCTTTCAAGAGACCTTTGACTCTGTCTCAGAAAGAGTTCA 1082  
Db 1021 GATTTCTCTCAGACATGTCTTTCAAGAGACCTTTGACTCTGTCTCAGAAAGAGTTCA 1080  
Qy 1083 ATTTTCAACAGAGAAAGTAAACAGGAGCTTTTAAACAAAGACCAACCAATCTAGCCTTG 1142  
Db 1081 ATTTTCAACAGAGAAAGTAAACAGGAGCTTTTAAACAAAGACCAACCAATCTAGCCTTG 1140  
Qy 1143 GAACAAACCAAGAGACCCACAGGTGAGGATGTTTCAAGATTAACAACTTTGTA 1193  
Db 1141 GAACAAACCAAGAGACCCACAGGTGAGGATGTTTCAAGATTAACAACTTTGTA 1191

## RESULT 4

US-09-841-683-12

; Sequence 12, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 1675

; TYPE: DNA

; ORGANISM: homo sapiens

; US-09-841-683-12

Query Match 78.3%; Score 1162.6; DB 4; Length 1675;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCATGGAGGGAACACTTCAAGAAAACCCAGTGTGTTGATGAAATGAAGATGTCAC 60  
Db 411 CCATGGAGGCAACACTTCAAGAAAACCCAGTGTGTTGATGAAATGAAGATGTCAC 470  
Qy 61 TTGACCACTTTGAAATTTTGGAGCCATTTGGGAAGCGAGTTTGGGAGGCTGTCAT 120  
Db 471 TTGACCACTTTGAAATTTTGGAGCCATTTGGGAAGCGAGTTTGGGAGGCTGTCAT 530  
Qy 121 TACAGAAGATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAACAAAGTGG 180  
Db 531 TACAGAAGATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAACAAAGTGG 590  
Qy 181 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGAACTCCAGATCATCGAGGCTCGAGC 240  
Db 591 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGAACTCCAGATCATCGAGGCTCGAGC 650  
Qy 241 ACCCTTTCTGTTTAAATTTCTGTTGTTTCTTCAAGATGAGGAGACATGTTTCATG 300  
Db 651 ACCCTTTCTGTTTAAATTTCTGTTGTTTCTTCAAGATGAGGAGACATGTTTCATG 710  
Qy 301 TGGACCTCTCTGCTGGGTGAGACCTGCGTTTATCACCTGCAACAGAGCTCCACTTCA 360

Db 711 TGGACCTCTCTGCTGGGTGAGACCTGCGTTATCACTGCAACAGAACTCCACTTCAAG 770  
Qy 361 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTCACTGSCCTGAGTACTCTGCAAGACC 420  
Db 771 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTCACTGSCCTGAGTACTCTGCAAGACC 830  
Qy 421 AGCGATCAATTCACAGGATATGAAGCTGACATATTTTACTTGAACAACTGGGCAAG 480  
Db 831 AGCGATCAATTCACAGGATATGAAGCTGACATATTTTACTTGAACAACTGGGCAAG 890  
Qy 481 TGCACATCAGAGATTTCAACATTTGCTGCGATGTGCTCCAGGAGAGACACAGATTACCA 540  
Db 891 TGCACATCAGAGATTTCAACATTTGCTGCGATGTGCTCCAGGAGAGACACAGATTACCA 950  
Qy 541 TGGCTGGCAACCAAGCTTTACATGCACTGAGATGTTTCAAGCTCCAGAAAGAGAGAGCT 600  
Db 951 TGGCTGGCAACCAAGCTTTACATGCACTGAGATGTTTCAAGCTCCAGAAAGAGAGAGCT 1010  
Qy 601 ATTCTTTGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 1011 ATTCTTTGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070  
Qy 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGAAATTTGTACACAGTTTGAGA 720  
Db 1071 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGAAATTTGTACACAGTTTGAGA 1130  
Qy 721 CGACTGTTGTAACCTTACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Db 1131 CGACTGTTGTAACCTTACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1190  
Qy 781 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGCTCAGAACTTCCCGT 840  
Db 1191 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGCTCAGAACTTCCCGT 1250  
Qy 841 ATATGAATGATATAAACTGGGATGAGTGTGTTTTCAGAGAGGCTCAATTCAGGTTTCA 900  
Db 1251 ATATGAATGATATAAACTGGGATGAGTGTGTTTTCAGAGAGGCTCAATTCAGGTTTCA 1310  
Qy 901 CTATATAAGGAGGCTGATGTTGATGCTTCTGATGCTTCTGATGCTGAGGAAATGATTTGG 960  
Db 1311 CTATATAAGGAGGCTGATGTTGATGCTTCTGATGCTTCTGATGCTTCTGAGGAAATGATTTGG 1370  
Qy 961 CCACACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGAGAGAGATATGAGGAAAT 1020  
Db 1371 CCACACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGAGAGAGATATGAGGAAAT 1430  
Qy 1021 GCGATTTCTTCTCAGACATGTCTTCTTCAAGAGACCTTTGACTCTCTCAGAGAGGAGTTCA 1080  
Db 1431 GCGATTTCTTCTCAGACATGTCTTCTTCAAGAGACCTTTGACTCTCTCAGAGAGGAGTTCA 1490  
Qy 1081 TAAATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACAACTTCTAGCCT 1140  
Db 1491 TAAATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACAACTTCTAGCCT 1550  
Qy 1141 TGAACAAACCAAGACCCCAAGGTGAGGATGCTGAGAAATAACA 1185  
Db 1551 TGAACAAACCAAGACCCCAAGGTGAGGATGCTGAGAAATAACA 1595

## RESULT 5

US-09-841-683-8

; Sequence 8, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683



```

; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-583-8

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Query Match	78.2%	Score 1160.6;	DB 4;	Length 1224;
Best Local Similarity	98.8%	Pred. No. 0;		
Matches 1169;	Conservative	0;	Mismatches 14;	Indels 0;
Gaps	0;			

Qy	3	ATGGGAGGAAACATTTCAAGAAAACCAACGATGTTTGATGAAATGAAGATGTCAACTTTT	62
Db	1	ATGGGAGCCAAACATTTCAAGAAAACCAACGATGTTTGATGAAATGAAGATGTCAACTTTT	60
Qy	63	GACCACATTTTGAAATTTTTCGAGGCCAATGGGAAAGCGATTTTGGGAGGTCATGATTGTA	122
Db	61	GACCACATTTTGAAATTTTTCGAGGCCAATGGGAAAGCGATTTTGGGAGGTCATGATTGTA	120
Qy	123	CAGAAGAATGATATCAAGAAGATGTGCGCAATGAAGTACATGAATATAAATAAAGTGC	182
Db	121	CAGAAGAATGATATCAAGAAGATGTGCGCAATGAAGTACATGAATATAAATAAAGTGC	180
Qy	183	GAGGCGCAATGAAAGTGAGAAATGCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC	242
Db	181	GAGGCGCAATGAAAGTGAGAAATGCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC	240
Qy	243	CCTTTCCCTGGTTAAATTTGTGCTATTTCTTCCAAGATGAGGAAGCATGTCTCATGGTGGTG	302
Db	241	CCTTTCCCTGGTTAAATTTGTGCTATTTCTTCCAAGATGAGGAAGCATGTCTCATGGTGGTG	300
Qy	303	GACCTCTGCTGGGTGGAGACCTCGGTTATACCTGCAACAGAACGTCACATTCAAAGGAA	362
Db	301	GACCTCTGCTGGGTGGAGACCTCGGTTATACCTGCAACAGAACGTCACATTCAAAGGAA	360
Qy	363	GAACAAGTGAAGCTTTCATCTGTGAGCTGTGTCATGGCCCTGGGACTACTTCGACGAACCG	422
Db	361	GAACAAGTGAAGCTTTCATCTGTGAGCTGTGTCATGGCCCTGGGACTACTTCGACGAACCG	420
Qy	423	CGCATATTTCA CAGGGATATGAAGCCTGACAAATATTTTACTTTGACGAACATGGGCA	482
Db	421	CGCATATTTCA CAGGGATATGAAGCCTGACAAATATTTTACTTTGACGAACATGGGCA	480
Qy	483	CACATCA CAGATTTCAACATTTGCTGCGATGTGCCCAGGGAGACACAGATTAACAAC	542
Db	481	CACATCA CAGATTTCAACATTTGCTGCGATGTGCCCAGGGAGACACAGATTAACAAC	540
Qy	543	GCTGGCACCAAGCCTTACATCGCACCTTGAGATGTTTCAGCTCCAGAAAGGAGCAGGCTAT	602
Db	541	GCTGGCACCAAGCCTTACATGGCACTGAGATGTTTCAGCTCCAGAAAGGAGCAGGCTAT	600
Qy	603	TCCTTTGCTGTGTGACTGGTGTCTCCCTGGGAGTGACGCATATGAATCTGCTGAGAGCCGG	662
Db	601	TCCTTTGCTGTGTGACTGGTGTCTCCCTGGGAGTGACGCATATGAATCTGCTGAGAGCCGG	660
Qy	663	AGACCGTATCATATTTGGCTCAGTACTTCCAGCAAGGAAATGTGTACACACGTTTGAGACG	722
Db	661	AGACCGTATCATATTTGGCTCAGTACTTCCAGCAAGGAAATGTGTACACACGTTTGAGACG	720
Qy	723	ACTGTTGTAACTTACCTTCTGCTCTGGTCCAGGAAATGGTGTCACTTCTTAAAAAGCTA	782
Db	721	ACTGTTGTAACTTACCTTCTGCTCTGGTCCAGGAAATGGTGTCACTTCTTAAAAAGCTA	780
Qy	783	CTCGAACTTAATCCAGACCAACGATTTTCTCAGTTATCTGATATCCAGAACTTCCCGTAT	842
Db	781	CTCGAACTTAATCCAGACCAACGATTTTCTCAGTTATCTGATATCCAGAACTTCCCGTAT	840

```

RESULT 6
US-09-841-683-6
; Sequence 6, Application US/09841693
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Doncho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human K
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,693
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 711
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-6

```

Query Match	44.2%	Score 656.2	DB 4	Length 711
Best Local Similarity	99.5%	Pred. No. 3.5e-197		
Matches 658	Conservative 0	Mismatches 137	Indels 0	Gaps 0
Qy	3	ATGGGCGCAACACTTCAAGAAACACCAACCACTGTTTGATGAAATGAAGATGTCAACTTT	62	
Db	1	ATGGGCGCAACACTTCAAGAAACACCAACCACTGTTTGATGAAATGAAGATGTCAACTTT	60	
Qy	63	GACCACTTTGAAATTTTCGAGCCATTTGGGAAAGCGCATTTTGGGAGGTCGCAATGTA	122	
Db	61	GACCACTTTGAAATTTTCGAGCCATTTGGGAAAGCGCATTTTGGGAGGTCGCAATGTA	120	
Qy	123	CAGAAGAATGATACCAAGAAGATGTGGCGCAATGAAGTACATGAATAACAAAAGTGCCTG	182	
Db	121	CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAACAAAAGTGCCTG	180	
Qy	183	GAGCGCAATGAAGTGAAGATGTCTTCAAGGAATCCAGATCATCGAGGGTCTGGAGCAC	242	
Db	181	GAGCGCAATGAAGTGAAGATGTCTTCAAGGAATCCAGATCATCGAGGGTCTGGAGCAC	240	
Qy	243	CTTTCTCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCAATGGTGGTG	302	



Db 157 GCCATGAAGTACATGAACAAGCAGCAGTGCATCGAGCGGAGGTCGCAACCTCTTC 216  
QY 210 AAGGAACCTCAGATCATGAGGCTGAGAGCACCCTTTCTCTGTTAAATTTGGGATTC 269  
Db 217 CGGAGCTGGAGTCTCGAGGAGATCGAGCAGCTTCTCTGTTGAACCTCTGTAATCC 276  
QY 270 TTCCAAGATGAGGAAGACATGTTCTATGTTGGTGGACCTCTCTCTGTTGGAGCCTGGT 329  
Db 277 TTCCAGGACGAGGAGCAGTTCATGTCGTGGACCTGTAATCTGGGCGGAGCCTGGC 336  
QY 330 TATCACTCTGCAACAGACCTCCACTTCAAGGAAGAAACAGTAGTCACTTCTATCTGTAG 389  
Db 337 TACCACTCTGCAAGACCTGAGTTCCTCCGAGGACAGCTGAGCTGTACATCTGCGAG 396  
QY 390 CTGGTCATGGCCCTGAGCTACTCTGAGACACGAGCAGCTCATTCACAGGATATGAGCT 449  
Db 397 ATGGCACTGGCTCTGGACTACTCTGGCGGCCAGCAGCATCATCCACAGAGATGTCAAGCT 456  
QY 450 GACATATTTTACTTGAAGCAATGCGGACGTCACATCACAGATTTCAACATTTCTGCTGG 509  
Db 457 GACACATTTCTCTGATGAGAGGACATGACACACCTGACGACCTTCAACATTTGCCACC 516  
QY 510 ATGCTGCCAGGAGACACAGATTAACCATGCTGGCAGCAGCCTTTACATGCACT 569  
Db 517 ATCATCAAGGACGGGAGCGGCGGCGCATTTAGCAGGACACCAAGCGGTACATGCTCG 576  
QY 570 GAGATGTTCACTC-----CAGAAAGGAGCAGGCTATTTCTTCTGTTGACTGGTGG 623  
Db 577 GAGATGTTCACTCTTTTGTCAACGCGGAGCAGGCTACTCTCTGAGTGGACTGGTGG 636  
QY 624 TCCCTGGGAGTCAAGCATATGAACTGCTGAGAGCGGAGACCGTATCATATTCGCTCC 683  
Db 637 TCGGTGGGGGTGATGGCTATGAGCTGCTGCGAGATGAGGCGCTTATGACATCACTCC 696  
QY 684 AGTACTTCCAGAGAAATTTGACACAGTTTGAAGCAGCTGTTGTAATTTACCTCTCT 743  
Db 697 AGCAACGCGGTGGAGTCCCTGCTGAGCTGTTTTCAGCAGCGTGGCGTTCAGTATGTC 756  
QY 744 GCCTGTCACAGGAATGTTGTCATTTCTTAAAGCTACTGCAACCTTAATCCAGACCA 803  
Db 757 AGTGGTCCAGGAGATGTTGCTTGTGCGGAAGCTCTCTCACTGTGAACCCCGAGCAC 816  
QY 804 CGATTTCTCAGTATCTGATGTCAGAACTTCCCGTATATGAATGATATAAATCTGGAT 863  
Db 817 CGCTCTCAGCTCCAGACCTGAGGAGCGGCGGCGCTGGCGGCTGCTGTGGAC 876  
QY 864 GCAGTTTTTCAAGAGGCTCATTCAGGTTTTCAATTCCTTAATAAGGCGAGGCTGAATGT 923  
Db 877 CACCTGAGCGAGAGGAGGAGGAGCGGCGCTTCTGTCGCCCAACAAAGGCGCTCTG 936  
QY 924 GATCTACCTTTGAACTTGAAGAAATGATTTTGGAGTCCAAACCTTACATGAAGAAA 983  
Db 937 GACCCACCTTTGAGCTGAGGAGATGATCTTGGAGTCCAGGCGCTGTCACAGAGAG 996  
QY 984 AAGCGTCTGGCAAGAGAA-----GAAGGATATGAGGAATGCGATTTCTTCAGACA 1037  
Db 997 AAGGCTCTGCGCAAGAAAGTCCCGGAGACACAGCAGGAGCAGCTCCAGTCCGAGAT 1056  
QY 1038 TGTCTTTTCAAGAGACCTTGAATCTGTCAGAGAGGATTCATATTTTCAACAGAGAA 1097  
Db 1057 GACTATCTTCAAGACTGCTCGATGCCATCCAGCAGACTTCTGATTTTTTAACAGAGAA 1116  
QY 1098 AAGTAACAGG 1109  
Db 1117 AAGCTGAAGAG 1128

## RESULT 9

US-09-799-875-13

; Sequence 13, Application US/09799875

; Patent No. 6638721

; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses  
; FILE REFERENCE: 35800/209996  
; CURRENT APPLICATION NUMBER: US/09/799,875  
; CURRENT FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: 60/182,059  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 09/659,287  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 1826  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (17)...(1273)  
US-09-799-875-13

Query Match 32.4%; Score 481.6; DB 4; Length 1826;  
Best Local Similarity 66.5%; Pred. No. 1.2e-141;  
Matches 726; Conservative 0; Mismatches 354; Indels 12; Gaps 2;

QY 30 CCAGTGTGATGAATAATGAAGATGTCACTTTGACCACTTTGAAATTTTGGAGCCATT 89  
Db 53 CCGGTGTTTGACGACAGGAGGACGTGAACCTTCGACCACTTCCAGATCTCTTGGGCCATT 112  
QY 90 GGGAAAGGACGCTTTGGGAGGCTGTCATTGTACAGAAGAATGATACCAGAAGATGTGC 149  
Db 113 GGGAAAGGACGCTTTGGGAGGCTGTCATTGTGCGAAGCGGACACGAGAGATGTAC 172  
QY 150 GCAATGAAGTACATGAATAAACAAGTGCCTGGAGCGCAATGAAGTGAAGAAATGCTTC 209  
Db 173 GCCATGAATACATGAACAAGCAGCAGTGCATCGAGCGCAGAGGTCCGCAACGCTTTC 232  
QY 210 AAGGAATCCAGATCATGACGGGTCTGGAGCAGCCTTCTCTGTTAAATTTGGGTATTC 269  
Db 233 CGGAGCTGGAGATCTCTGAGGAGATCGAGCAGCTCTTCTGTTGAACCTCTGTTACTCC 292  
QY 270 TTCCAAGATGAGGAAGACATGTTCTATGTTGGTGGACCTCTCTGCTGGTGGAGCCTGGT 329  
Db 293 TTCCAAGATGAGGAAGACATGTTCTATGTTGGTGGACCTCTCTGCTGGTGGAGCCTGGC 352  
QY 330 TATCACTCTGCAACAGACGCTCCACTTCAAGGAAGAAACAGTGAAGCTCTTCACTGTGAG 389  
Db 353 TACCACCTGACAGAGACGTCAGTTCTCCGAGGACACGCTGAGGCTGTACATCTGCGAG 412  
QY 390 CTGGTCATGGCCCTGGACTACTCTGAGAACCGAGGACATTCACAGGATATGAGCT 449  
Db 413 ATGGCACTGGCTCTGGACTACTCTGCGCGCCAGCAGCATCATCCACAGAGATGTCAAGCT 472  
QY 450 GACATATTTTACTTGAAGAACATGCGGACATGCGACATCACAGATTTCAACATTTCTGCTGG 509  
Db 473 GACACATTTCTCTGATGAGAGGACATGCAACACCTGACCGACTTCAACATTTGCCACC 532  
QY 510 ATGCTGCCAGGAGACACAGATTAACCATGCTGGCTGGACACCAAGCCTTACATGAGCACT 569  
Db 533 ATCATCAAGGACGGGAGCGGCGGAGCGGCAATTTAGCAGGACACCAAGCGGTACATGCTCG 592  
QY 570 GAGATGTTCACTC-----CAGAAAGGAGCAGGCTATTTCTTGTGCTGTTGACTGGTGG 623  
Db 593 GAGATCTTCCACTCTTTTGTCAACGCGGAGACCGGCTACTCTCTGAGGTGACTGGTGG 652  
QY 624 TCCCTGGGAGTCAAGGATATGAATGCTGAGAGCGCGGAGACCGTATCATATTTGCTGCC 683  
Db 653 TCGGTGGGGGTGATGGCTTATGAGCTGCTGCGAGGATGAGGCGCTTATGACATCACTCC 712  
QY 684 AGTACTTCCAGAGAAATTTGACACAGTTTGAAGCAGCTGTTGTAATTTACCTCTCT 743

713	AGCAACGCGTGAGTCCCTGTGTGCAGCTGTTACAGCACCGTGAGCGTCCAGTATGTCCCC	772
744	GCCTGTGTACAGGAATGGTGTACATCTTTAAAGACTACTCGAACTAATCAGACCAA	803
773	ACGTGTGTCCAAGGAGATGTGGCTTGTGCGGAAGCTCCTCACTGTGAACCCGAGCAC	832
804	CGATTTTCTCAGTTATCTGATGTGCAGAACTTCCCCTATATGAATGATATAACTTGGAT	863
833	CGGCTCTCCAGCCTCAGGACGTGCAGGACGCCCCGGCGCTGGCCGGCTGTGTGGGAC	892
864	GCAGTTTTTTCAGAAAGGCTCATTTCCAGGTTTCATTCTCTAAATAAAGCGCAGGCTGAATGT	923
893	CACCTGAGCGAGAAAGGGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTCTGCCTGC	952
924	GATCTCACTTTTGAACTTCAGGGAATGATTTTGGAGTCCAAACCTCTCATAGAAGAAA	983
953	GACCCACCTTTTGAGCTGGAGGAGATGATCTTGGAGTCCAGGCCCTGCACAGAAGAAG	1012
984	AAGCGTCTGCCAAGAGGA-----GAAGGATATGAGGAATGCCATTTCTTCAGACA	1037
1013	AAGCGTCTGGCCAAAGAACAAAGTCCCGGGAACACAGCAGGGACAGCTCCCGTCCGAGAT	1072
1038	TGTCCTTTCTCAAGCACCTTGACTCTGTGCCAAGGAGTTCAATAATTTTCAACAGAA	1097
1073	GACTATCTTTCAGACTGCGCTCGATGTCATCCAGCAAGACTTCTGTGATTTTACAGAGAA	1132
1098	AAAGTAAACAGG	1109
1133	AAGCTGAAGAGG	1144

**RESULT 10**

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US-09-819-607-1
; Sequence 1, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Human
US-09-819-607-1

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329	AGGAGGACATGTTTCATGGTCTGAGCACTGCTACTGGGGGGGAGCACTGGCGCTTACCACTGC	388
340	AAACAGAACGTCCACTTCAAGGAAGAAAACAGTGAAGCTCTTCACTGTGTGAGCTGGTCATGG	399
389	AGCAGAAAGTGCAGTCTTCCGAGGACACGGTGAAGCTGTACATCTGCGAGATGGCACTGG	448
400	CCCTGGACTTACCTGCAGAACACAGCCCATCTTCAAGGGATATGAAGCTCGACATATTT	459
449	CTCTGGACTACTTGGCGGCGCAGCACATCATCCACAGAGATGTCAAGCTCTGACCAATTC	508
460	TACTTTGACCAACATGGGACGCTGCACATCACAGATTTCAACATTTGCTGCGATGCTGCCCA	519
509	TCCTGGATGAGAGGACATGCACACCTGACCGACTTCAACATTTGCCACCATCATCAAGG	568
520	GGGAGACACAGATTAACCACTATGGCTGGGACCAAGCCTTACATGGCACTGAGATGTTCA	579
569	ACGGGGAGCGGCGCAGCGGCAATTAGCAGGACCAAGCCGTACATGGCTCCGGAGATCTTCC	628
580	GGTC-----CAGAAAAAGGACAGGCTATTCTCTTTGTTGTTCACATGGTGGTCCCTGGGAG	633
629	ACTCTTTTGTCAACGGCGGGAACCGGCTACTCTCTTCAGGTGACATGTGTGCTGGTGGGG	688
634	TGACGGCATTATGAATGCTGTGAGAGCCGGAGACCGTATCATATTCGCTCCAGTACTTCCA	693
689	TGATGGCCTATGAGTCTGTCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCG	748
694	GCAGGAATTTGTACACAGTTTGAGACGACTGTTGTAACTTACCGTCTTGCTGGTGGTCAAC	753
749	TGGAGTCCCTGGTGCAGCTGTTTTCAGCACCGTGAGCGTCCAGTATGTGCCACATGGTCCA	808
754	AGCAATGTGTGTCATCTTCTTAAAAAGCTACTCGAACCTTAATCCAGACCAACGATTTTCTC	813
809	AGGAGATGTGTGCTTGTCTGCGGAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCA	868
814	AGTTATCTGATGTCCAGAACTTCCCGGTATATGAATGATATAAACTGGGGATGCAAGTTTTTC	873
869	GCCTCCAGGACGTGCAGGCAGCCCGCGCGCTGGCGCGGTGCTGTGGGACCACTTGAGCG	928
874	AGNAGAGGCTCATTTCCAGGTTTCATTCCTAATAAAGGCAGGCTGAATTCGTGATCCTPACCT	933
929	AGNAGAGGTGGAGCGGGCTTCTGGTCCCAACAAAGGCCGTCTGCATCGGACCCCACTT	988
934	TTTGAACTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAAAAAGCGCTGG	993
989	TTTGAGCTGGAGGAGATGATCTCTGGAGTCCAGGCCCTGCAACAAGAAAGAGAGCGCTGG	1048
994	CAAAAGAGA-----GAAGGATATGAGGAATGCGATTTCTTCTCAGACATGCTCTTCTTC	1047
1049	CCAAGAAACAGTCCCGGGAACACAGCAGGGAACAGCTCCCGAGTCCGAGAAATGACTATCTTC	1108
1048	AAAGAGCACTTGACTCTGTCTCAGAGGAGTTCATATTTTCAACAGAGAAAAAGTAAACA	1107
1109	AAAGCTGCTTCGATGCCATCCAGCAAGACTTTCGTGATTTTTTAAACAGAGAAAGCTGAAGA	1168
1108	GG 1109	
1169	GG 1170	

```

RESULT 11
US-09-801-876B-3
; Sequence 3, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEAR
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(148567)
; OTHER INFORMATION: n = A,T,C or G
US-09-801-876B-3

Query Match      24.5%; Score 363.4; DB 4; Length 148567;
Best Local Similarity 98.4%; Pred. No. 7.6e-103;
Matches 367; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1097 AAAAGTAAACAGGGACTTTAAACAAAGACCAACCAATCTAGCCTTGGAAACCAAGA 1156
DB 146198 AAGAGTAAACAGGGACTTTAAACAAAGACCAACCAATCTAGCCTTGGAAACCAAGA 146257

QY 1157 CCCAAGGTGAGGATGTCAGAAATACAACTTGTAAAGGCTCATGTCTTCTTGGG 1216
DB 146258 CCCAAGGTGAGGATGTCAGAAATACAACTTGTAAAGGCTCATGTCTTCTTGGG 146317

QY 1217 ACAATCTCATGCCAGAACTTCTAATTTACATATGTCAAGAAAGCTGACAGTAGTCTTG 1276
DB 146318 ACAATCTCATGCCAGAACTTCTAATTTACATATGTCAAGAAAGCTGACAGTAGTCTTG 146377

QY 1277 CCACCTCCACACACCATGACTTAGAAAAATGTGAATGAATATATTTCAAAAAAGGCGACACA 1336
DB 146378 CCACCTCCACACACCATGACTTAGAAAAATGTGAATGAATATATTTCAAAAAAGGCGACACA 146437

QY 1337 ACACAGTGAAGGTCCTGGGCTGAGCTCCTGGAAAGTCAATTCACATCAATCAACTGTG 1396
DB 146438 ACACAGTGAAGGTCCTGGGCTGAGCTCCTGGAAAGTCAATTCACATCAATCAACTGTG 146497

QY 1397 TGATCTAGAGCAAGTCACTTAGCCACTTCTGTCTTTTACTTTTATCTTAAATGAGA 1456
DB 146498 TGATCTAGAGCAAGTCACTTAGCCACTTCTGTCTTTTACTTTTATCTTAAATGAGA 146557

QY 1457 GGGTTATACTAAA 1469
DB 146558 GGGTTATACTAGA 146570

RESULT 12
US-10-254-869-3
; Sequence 3, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(148567)
; OTHER INFORMATION: n = A,T,C or G
US-10-254-869-3

Query Match      24.5%; Score 363.4; DB 4; Length 148567;
Best Local Similarity 98.4%; Pred. No. 7.6e-103;
Matches 367; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1097 AAAAGTAAACAGGGACTTTAAACAAAGACCAACCAATCTAGCCTTGGAAACCAAGA 1156

; SEQ ID NO 3
; LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(148567)
; OTHER INFORMATION: n = A,T,C or G
US-09-801-876B-3

Query Match      24.5%; Score 363.4; DB 4; Length 148567;
Best Local Similarity 98.4%; Pred. No. 7.6e-103;
Matches 367; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1097 AAAAGTAAACAGGGACTTTAAACAAAGACCAACCAATCTAGCCTTGGAAACCAAGA 1156
DB 146198 AAGAGTAAACAGGGACTTTAAACAAAGACCAACCAATCTAGCCTTGGAAACCAAGA 146257

QY 1157 CCCAAGGTGAGGATGTCAGAAATACAACTTGTAAAGGCTCATGTCTTCTTGGG 1216
DB 146258 CCCAAGGTGAGGATGTCAGAAATACAACTTGTAAAGGCTCATGTCTTCTTGGG 146317

QY 1217 ACAATCTCATGCCAGAACTTCTAATTTACATATGTCAAGAAAGCTGACAGTAGTCTTG 1276
DB 146318 ACAATCTCATGCCAGAACTTCTAATTTACATATGTCAAGAAAGCTGACAGTAGTCTTG 146377

QY 1277 CCACCTCCACACACCATGACTTAGAAAAATGTGAATGAATATATTTCAAAAAAGGCGACACA 1336
DB 146378 CCACCTCCACACACCATGACTTAGAAAAATGTGAATGAATATATTTCAAAAAAGGCGACACA 146437

QY 1337 ACACAGTGAAGGTCCTGGGCTGAGCTCCTGGAAAGTCAATTCACATCAATCAACTGTG 1396
DB 146438 ACACAGTGAAGGTCCTGGGCTGAGCTCCTGGAAAGTCAATTCACATCAATCAACTGTG 146497

QY 1397 TGATCTAGAGCAAGTCACTTAGCCACTTCTGTCTTTTACTTTTATCTTAAATGAGA 1456
DB 146498 TGATCTAGAGCAAGTCACTTAGCCACTTCTGTCTTTTACTTTTATCTTAAATGAGA 146557

QY 1457 GGGTTATACTAAA 1469
DB 146558 GGGTTATACTAGA 146570

RESULT 13
US-09-394-455-3
; Sequence 3, Application US/09394455
; Patent No. 6531305
; GENERAL INFORMATION:
; APPLICANT: Witman, George F.
; APPLICANT: San Agustin, Jovenal
; APPLICANT: Lezyk, John D.
; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: 07917/078001
; CURRENT APPLICATION NUMBER: US/09/394,455
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/099,771
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1008)
US-09-394-455-3

Query Match      8.9%; Score 132.6; DB 4; Length 1008;
Best Local Similarity 54.1%; Pred. No. 2e-31;
Matches 323; Conservative 0; Mismatches 259; Indels 15; Gaps 2;

QY 54 GTCAACTTTGACCACTTTGAAATTTTGGAGCCATTGGGAAGGCGACTTTTGGGGAGTTC 113
DB 70 GCCCACTTGGATCAGTTTGAACGAACTCAAGACCCCTCGGCGCTCCCTTCGGGGGGGTG 129

QY 114 TGCATTGTACAGAAAGATGATACCAAGAAAGTGTGCGCAATGAAGTACATGAATAAACA 173
DB 130 ATGCTGTGAAACACAGAGGACCGGNAACCACTATGCCATGAAGATCCTCGACAAACAG 189

QY 174 AAGTGCCTGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAATCTCCAGATCATGAGGGT 233
DB 190 AAGGTGTGAAACTGAAACAGATCGAACACACACCCTGAATGAAAGCGCATCTGCAAGCT 249

QY 234 CTGAGGACCCCTTCTGTTTAAATTTGTGGTATTTCTTCCAGATGAGGAGAGCATGTC 293
DB 250 GTCAACTTTCCGTTCTCGTCAAACTCGAGTTCTCTTCAAGGCAACTCAAACTTATAC 309
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Qy	354	TTCAAGGAAGAAACAGTGAAGCTCTTCATCTGTGAGTGGTCATGGCCCTGGACTACCTG	413
Db	495	TTCACTGAGCCCATGCCCGTTTCTACGGGGCCGAGATCGTCTGACCTTTGAGTATCTG	554
Qy	414	CAGAACCGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTTGACGAACAT	473
Db	555	CACTCGCTGGATCTCATCTACAGGGACCTGAAGCCGGAGATCTGCTCATTGACCCAGCAG	614
Qy	474	GGGCACGTGCACATCACAGATTTCACATTTGCTGCGATGCTGCCCGAGGGAGACACAGATT	533
Db	615	GGCTACATTCAGGTGACAGACTTCGGTTTCGCCAA-----CGCGTGAAGGGCCGCACT	668
Qy	534	ACCACCATGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGCTCCAGAAAGGA	593
Db	669	TGGACCTTGTGGGCACCCCTGAGTACCTGGCCCTGAGATTATCTGAGCAA-----721	
Qy	594	GCAGCTATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACCGGCATATGAAGCTG	650
Db	722	--AGGCTAACACAGGCCGTGGACTGGTGGGCCCTGGGGGTTCTTTATCTATGAATG	776

Search completed: June 26, 2004, 23:09:37  
 Job time : 99 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:01:41 ; Search time 467 Seconds  
(without alignments)  
13508.724 Million cell updates/sec

Title: US-10-667-442-1  
Perfect score: 1485  
Sequence: 1 ccatgggagggacactctca.....taaaaaaaaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747756

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseq1980s:\*  
2: geneseq1990s:\*  
3: geneseq2000s:\*  
4: geneseq2001as:\*  
5: geneseq2001bs:\*  
6: geneseq2002as:\*  
7: geneseq2003as:\*  
8: geneseq2003bs:\*  
9: geneseq2003cs:\*  
10: geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1485	100.0	1485	7	ABs55499 CDNA enco
2	1485	100.0	1485	8	ACA62840 CDNA enco
3	1228.6	82.7	1281	6	AA170704 Human 149
4	1188.2	80.0	1594	4	AH46891 CDNA enco
5	1188.2	80.0	1594	6	AH46891 Human PKI
6	1186.2	79.9	1191	6	AAD23679 Novel hum
7	1162.6	78.3	1675	6	AAD23680 Novel hum
8	1160.6	78.2	1224	6	AAD23678 Novel hum
9	831.2	56.0	981	4	AS06704 Polynucle
10	672.8	45.3	678	4	ABA08463 Human Ser
11	656.2	44.2	711	6	AAD23677 Novel hum
12	655.2	44.1	678	6	AAD23676 Novel hum
13	540.8	36.4	1587	6	ABQ61051 Serine/th
14	540.8	36.4	3224	4	AAP44625 Novel pro
15	540.8	36.4	3224	7	ADA19317 Human ins
16	540.8	36.4	3224	7	ACC72764 Human can
17	540.8	36.4	3224	9	AD38374 Human pro
18	516.4	34.8	3244	4	AA546210 Human DNA
19	516.4	34.8	3244	7	ABX78813 Human PRO
20	516.4	34.8	3244	7	ACA75785 Novel hum
21	516.4	34.8	3244	7	ACA71265 Human sec
22	516.4	34.8	3244	7	ACC87793 Human sec
23	516.4	34.8	3244	7	ACC87179 Human sec

24	516.4	34.8	3244	7	ACD04352	Human sec
25	516.4	34.8	3244	7	ACA69683	CDNA enco
26	516.4	34.8	3244	7	ACA90528	Novel hum
27	516.4	34.8	3244	7	ACC89635	Human sec
28	516.4	34.8	3244	7	ACA98426	Novel hum
29	516.4	34.8	3244	7	ACA94068	Human sec
30	516.4	34.8	3244	7	ACD15461	Human sec
31	516.4	34.8	3244	7	ACD09048	Human sec
32	516.4	34.8	3244	7	ACC96968	Human sec
33	516.4	34.8	3244	7	ACF15689	Human sec
34	516.4	34.8	3244	7	ACF15689	Human PRO
35	516.4	34.8	3244	7	ACD03228	Novel hum
36	516.4	34.8	3244	7	ACD02043	Novel hum
37	516.4	34.8	3244	7	ACA92235	Novel hum
38	516.4	34.8	3244	7	ACA89660	CDNA enco
39	516.4	34.8	3244	7	ACA73670	Human sec
40	516.4	34.8	3244	7	ACA05985	Human sec
41	516.4	34.8	3244	7	ACA66819	CDNA enco
42	516.4	34.8	3244	7	ACF20394	Human sec
43	516.4	34.8	3244	7	ACF19780	Human sec
44	516.4	34.8	3244	7	ACD22068	Human sec
45	516.4	34.8	3244	7	ACF13233	Human sec

## ALIGNMENTS

## RESULT 1

ABs55499 ID ABS55499 standard; cDNA; 1485 BP.

XX AC ABS55499;

XX DT 14-JAN-2003 (first entry)

XX DE cDNA encoding human serine/threonine protein kinase-like kinase.

XX KW Human; kinase; serine/threonine kinase; immune response; transgenic;

XX KW gene therapy; chromosome 5; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT 5'UTR 1..2

FT CDS /\*tag= a

FT /\*tag= b

FT /\*tag= c

FT 3'UTR /product= "Serine/threonine protein kinase-like kinase"

FT 1194..1485

FT /\*tag= c

XX US2002127683-A1.

XX PD 12-SEP-2002.

XX PF 09-MAR-2001; 2001US-00801876.

XX PR 09-MAR-2001; 2001US-00801876.

XX PA (YEJ)/ YE J.

XX PA (YANC)/ YAN C.

XX PA (DFRA)/ DI FRANCESCO V.

XX PA (BEAS)/ BEASLEY E M.

XX PI Ye J, Yan C, Di Francesco V, Beasley EM;

XX DR WPI; 2003-028938/02.

XX DR P-ESDB; ABG70700.

XX PT Novel isolated human kinase peptide useful for treating disorder

XX PT characterized by absence of, in appropriate or unwanted expression of the

XX PT kinase protein, and as immunogens to raise antibodies.



Claim 4; Fig 1; 174pp; English.

The present invention relates to the isolation of a human kinase and the polynucleotide sequences encoding it. The human kinase of the invention is related to the serine/threonine kinase subfamily. The gene encoding the human kinase is located on chromosome 5. The polypeptide and polynucleotide sequences of the invention are useful for treating a disease or condition mediated by a human kinase. Both the polypeptide and polynucleotide sequences are useful as models for the development of human therapeutics, for identifying therapeutic proteins, as targets for development of human therapeutic agents, and as query sequences to perform a search against sequence data bases to identify other family members of related sequences. The polypeptide is useful to raise antibodies or to elicit another immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as markers for tissues in which the corresponding protein is preferentially expressed, in drug screening assays, in cell-based or cell-free systems, to identify compounds that modulate kinase activity of the protein in its natural state, or an altered form that causes the specific disease or pathology associated with the kinase, to screen a compound for the ability to stimulate or inhibit interaction between the kinase protein and a molecule that normally interacts with the kinase protein, and in pharmacogenomic analysis. The polynucleotide is useful for monitoring the effectiveness of modulating compounds on the expression or activity of the human kinase gene in clinical trials or in a treatment regimen, in diagnostic assays for qualitative changes in a human kinase nucleic acid that leads to a pathology, for testing an individual for a genotype that while not necessarily causing a disease, nevertheless affects the treatment modality, as antisense constructs to control human kinase gene expression in cells, tissues and organisms, for gene therapy in patients containing cells that are aberrant in human kinase gene expression, and to produce transgenic animals. The present sequence encodes a human kinase related to the serine/threonine protein kinase subfamily.

SQ Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;

Query Match	100.0%	Score 1485;	DB 7;	Length 1485;
Best Local Similarity	100.0%;	Prod. No. 0;		
Matches 1485;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCATGGGAGCGAAACACATCTCAAGAAAAACACACAGATGTTTGATGAAAAATGAAGATGTCAACT	60	
Db	1	CCATGGGAGCGAAACACATCTCAAGAAAAACACACAGATGTTTGATGAAAAATGAAGATGTCAACT	60	
Qy	61	TTGACCACTTTGAAATTTTGGAGGCCATTTGGGAAAGGCAGATTTTGGGGAGGTCTGCAATG	120	
Db	61	TTGACCACTTTGAAATTTTGGAGGCCATTTGGGAAAGGCAGATTTTGGGGAGGTCTGCAATG	120	
Qy	121	TACAGAAGAATGATACCAAGAAGAGATGTGGCCNATGAAGTACATGAATAAAACAAAGTGGC	180	
Db	121	TACAGAAGNATGATACCAAGAAGAGATGTGGCCNATGAAGTACATGAATAAAACAAAGTGGC	180	
Qy	181	TGGAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACCTCCAGATCATGCAAGGTCTGGAGC	240	
Db	181	TGGAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACCTCCAGATCATGCAAGGTCTGGAGC	240	
Qy	241	ACCTTTCTCGTTAAATTTGTGGTATTCTCTTCCAAGATGAGGAGACACATGTTTCATGGTGG	300	
Db	241	ACCTTTCTCGTTAAATTTGTGGTATTCTCTTCCAAGATGAGGAGACACATGTTTCATGGTGG	300	
Qy	301	TGGACCTTCTGCTGGTGGAGACCTGCGTTATTCACCTGCAACAGAACGTCCTCAAGG	360	
Db	301	TGGACCTTCTGCTGGTGGAGACCTGCGTTATTCACCTGCAACAGAACGTCCTCAAGG	360	
Qy	361	AAGAAACAGTGAAGCTTTCATCTGTGAGCTGGTCATGCGCCTGTGACATCTTCGTCAGAAC	420	
Db	361	AAGAAACAGTGAAGCTTTCATCTGTGAGCTGGTCATGCGCCTGTGACATCTTCGTCAGAAC	420	
Qy	421	AGCGCATCATTCACAGGGATATGAAGCCCTGCAATATTTTACTTCGACGAACATGGGCACG	480	
Db	421	AGCGCATCATTCACAGGGATATGAAGCCCTGCAATATTTTACTTCGACGAACATGGGCACG	480	

RESULT 2  
ACA62840  
ID ACA  
XX

AC ACA62840;  
 XX  
 DT 01-SEP-2003 (first entry)  
 XX  
 DE cDNA encoding human kinase.  
 XX  
 KW Human; ss; gene; kinase; gene therapy; cancer; inflammation; psoriasis;  
 KW arteriosclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 PH 5'UTR 1..2  
 FT /\*tag= a  
 FT 3..1193  
 FT /\*tag= b  
 FT /product= "Kinase"  
 FT 1194..1475  
 FT /\*tag= c  
 XX  
 XX US2003027307-A1.  
 XX  
 XX 06-FEB-2003.  
 XX  
 XX 26-SEP-2002; 2002US-00254869.  
 XX  
 XX 09-MAR-2001; 2001US-00801876.  
 XX  
 XX (APPL-) APPLERA CORP.  
 XX  
 XX Ye J, Yan C, Di Francesco V, Beasley EM;  
 XX  
 XX WPI; 2003-492035/58.  
 XX P-PSDB; ABU62276.  
 XX  
 XX New isolated human kinase proteins, useful for treating disorders  
 PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis  
 PT or psoriasis), or for development of human therapeutics and diagnostic  
 PT compositions.  
 XX  
 XX Claim 4; Fig 1; 185pp; English.  
 XX  
 XX The invention relates to a new isolated human kinase peptide. The human  
 CC kinase peptide and nucleic acid molecules are useful in the development  
 CC of human therapeutics and diagnostic compositions. The peptides are  
 CC useful for treating disorders (e.g. cancers, inflammations,  
 CC arteriosclerosis or psoriasis) characterised by an absence of,  
 CC appropriate, or unwanted expression of the kinase protein. These  
 CC molecules are particularly useful as models for developing human  
 CC therapeutic targets, identifying therapeutic proteins, or serving as  
 CC targets for the development of human therapeutic agents that modulate  
 CC kinase activity in cells and tissues that express the kinase. The  
 CC peptides are also useful for raising antibodies or eliciting an immune  
 CC response; as a reagent (including the labelled reagent) in assays  
 CC designed to quantitatively determine levels of the protein (or its  
 CC binding partner or ligand) in biological fluids; or as markers for  
 CC tissues in which the corresponding protein is preferentially expressed.  
 CC The agents identified are useful for treating a subject with a disorder  
 CC mediated by kinase pathway. The present sequence represents cDNA encoding  
 CC a human kinase  
 XX  
 SQ Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1485; DB 8; Length 1485;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCATGGGACGCAACTTCAAGAAAACCAACCAAGTGTGTTGATGAAAATGAAGATGTCAACT 60  
 DB 1 CCATGGGACGCAACTTCAAGAAAACCAACCAAGTGTGTTGATGAAAATGAAGATGTCAACT 60  
 QY 61 TTGACCACCTTTGAAATTTTGGAGCCATTTGGGAAAGGACATTTGGGGAGGTCTGCATTG 120

DB 61 TTGACCACCTTTGAAATTTTGGAGCCATTTGGGAAAGGACATTTTGGGGAGGTCTGCATTG 120  
 QY 121 TACAGAGAGATGATACCAAGAGATGTGGCAATGAAGTACATGAATAAACAAGTGCG 180  
 DB 121 TACAGAGAGATGATACCAAGAGATGTGGCAATGAAGTACATGAATAAACAAGTGCG 180  
 QY 181 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGGGTCTGGAGC 240  
 DB 181 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGGGTCTGGAGC 240  
 QY 241 ACCCTTTCTGGTTAATTTGTGTATTCCTTCAAGATGAGGAAGACATGTTTCAATGTGG 300  
 DB 241 ACCCTTTCTGGTTAATTTGTGTATTCCTTCAAGATGAGGAAGACATGTTTCAATGTGG 300  
 QY 301 TGGACCTCTCTGGTGGGAGACCTCGTTTATCACTTCAAGAAAGAGCTCCACTTCAAGG 360  
 DB 301 TGGACCTCTCTGGTGGGAGACCTCGTTTATCACTTCAAGAAAGAGCTCCACTTCAAGG 360  
 QY 361 AAGAAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGCGCCCTGGACTACCTGCAGAAC 420  
 DB 361 AAGAAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGCGCCCTGGACTACCTGCAGAAC 420  
 QY 421 AGCGCATCATTCACAGGGATATGAAGCTTGACATATTTTACTTGGACATATGGGACG 480  
 DB 421 AGCGCATCATTCACAGGGATATGAAGCTTGACATATTTTACTTGGACATATGGGACG 480  
 QY 481 TGCACATCACAGATTTCAACATTTGCTGCGATGCTGCCACAGGGAGACACAGATTACCA 540  
 DB 481 TGCACATCACAGATTTCAACATTTGCTGCGATGCTGCCACAGGGAGACACAGATTACCA 540  
 QY 541 TGGCTGGCAACCAAGCCTTACATGGCACTGAGATGTTTCAAGTCCAGAAAAGGAGCAGGT 600  
 DB 541 TGGCTGGCAACCAAGCCTTACATGGCACTGAGATGTTTCAAGTCCAGAAAAGGAGCAGGT 600  
 QY 601 ATTCTTTGCTGTGATGCTGCTGGAGTGGAGCGCATATGAATCTCTGAGAGGCC 660  
 DB 601 ATTCTTTGCTGTGATGCTGCTGGAGTGGAGCGCATATGAATCTCTGAGAGGCC 660  
 QY 661 GGAGACCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTGA 720  
 DB 661 GGAGACCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTGA 720  
 QY 721 CGACTGTTGTAATTTACCTTCTGCTGGTGCACAGAAATGGTGTCTTTTAAAAAGC 780  
 DB 721 CGACTGTTGTAATTTACCTTCTGCTGGTGCACAGAAATGGTGTCTTTTAAAAAGC 780  
 QY 781 TACTCGAACCTATCCAGACCAAGATTTTCTCAGTATCTGATGTCCAGAACTTCCCGT 840  
 DB 781 TACTCGAACCTATCCAGACCAAGATTTTCTCAGTATCTGATGTCCAGAACTTCCCGT 840  
 QY 841 ATATGAATGATATAAACTGGGATGCGATTTTTCAGAGAGGCTCATTTCCAGGTTTCATTC 900  
 DB 841 ATATGAATGATATAAACTGGGATGCGATTTTTCAGAGAGGCTCATTTCCAGGTTTCATTC 900  
 QY 901 CTAAATAAGCAGGCTGAATTTGATGCTTACCTTTGAACTTGAAGAAATGATTTTGAGT 960  
 DB 901 CTAAATAAGCAGGCTGAATTTGATGCTTACCTTTGAACTTGAAGAAATGATTTTGAGT 960  
 QY 961 CCAAACTCTTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAAT 1020  
 DB 961 CCAAACTCTTACATAAGAAAAAAGCGTCTGGCAAGAGGAGGATATGAGGAAAT 1020  
 QY 1021 GCGATTTCTTCTCAGACATGTCTTTTCAAGAGCACTTTGATCTGTCTCCAGAGAGGTTC 1080  
 DB 1021 GCGATTTCTTCTCAGACATGTCTTTTCAAGAGCACTTTGATCTGTCTCCAGAGAGGTTC 1080  
 QY 1081 TAATTTTCAACAGAGAAAAATGAAGAGGACTTTTAAACAAAGACACCAATCTAGCCT 1140  
 DB 1081 TAATTTTCAACAGAGAAAAATGAAGAGGACTTTTAAACAAAGACACCAATCTAGCCT 1140  
 QY 1141 TGGAAACCAACCAAGACCCCAAGGTGAGGATGTGAGATTAACAACTTTGTAAGAGGCTC 1200  
 DB 1141 TGGAAACCAACCAAGACCCCAAGGTGAGGATGTGAGATTAACAACTTTGTAAGAGGCTC 1200

QY 1201 ATGCTCTTCTTGGGACATCTCATGCCGAGAACTTCTAATTACATATGTCTCAAGAAAG 1260  
 DB |||||  
 QY 1201 ATGCTCTTCTTGGGACATCTCATGCCGAGAACTTCTAATTACATATGTCTCAAGAAAG 1260  
 DB |||||  
 QY 1261 CTGACAGTAGCTCTGCTGCTCCACACACCATCATCTAGAAATGTGAATGATATATTT 1320  
 DB |||||  
 QY 1261 CTGACAGTAGCTCTGCTGCTCCACACACCATCATCTAGAAATGTGAATGATATATTT 1320  
 DB |||||  
 QY 1321 CAAAAAGGAGCAGCAACACAGTGAAGGCTCTGGGCTGAGCTCTGGAAGTCAATTC 1380  
 DB |||||  
 QY 1321 CAAAAAGGAGCAGCAACACAGTGAAGGCTCTGGGCTGAGCTCTGGAAGTCAATTC 1380  
 DB |||||  
 QY 1381 ACATCAATCACTGTGATCTAGAGCACTTACAGCACTTCTAGCACTTCTGCTTACTTTA 1440  
 DB |||||  
 QY 1381 ACATCAATCACTGTGATCTAGAGCACTTACAGCACTTCTAGCACTTCTGCTTACTTTA 1440  
 DB |||||  
 QY 1441 TTTATCTAAATCAGAGGGTTATCTATAAAAAA 1485  
 DB |||||  
 QY 1441 TTTATCTAAATCAGAGGGTTATCTATAAAAAA 1485  
 DB |||||

RESULT 3  
 AAI70704  
 ID AAI70704 standard; cDNA; 1281 BP.  
 AC AAI70704;  
 XX  
 DT 04-FEB-2002 (first entry)  
 DE Human 14911 protein kinase cDNA.  
 KW Protein kinase; human; signal transduction; lung cancer; colon cancer;  
 OS brain cancer; breast cancer; gene therapy; diagnosis; ss.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 49..1239  
 FT /\*tag= a  
 XX  
 PN WO200181589-A2.  
 PD 01-NOV-2001.  
 PF 25-APR-2001; 2001WO-US013785.  
 XX  
 PR 25-APR-2000; 2000US-0199391P.  
 PR 15-JUN-2000; 2000US-0059392P.  
 XX  
 PA (WILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Meyers R, Hunter JJ;  
 XX  
 DR WPI; 2002-041408/05.  
 DR P-PSDB; AAM50334.  
 XX  
 PT Novel protein kinase nucleic acid molecules and the encoded proteins for  
 PT diagnosing and treating cellular proliferative, bone, immune,  
 PT cardiovascular, liver, pain or metabolic disorders and identifying  
 PT modulators.  
 XX  
 PS Claim 1(a); Fig 1A-B; 115pp; English.  
 XX  
 CC The present cDNA sequence, the coding region of which is also claimed,  
 CC encodes a novel human protein kinase, designated 14911 (see AAM50334).  
 CC This protein kinase plays a role in, or functions in, the transduction of  
 CC signals for cell proliferation, differentiation and apoptosis, modulating  
 CC the activity of one or more proteins involved in cellular growth or  
 CC differentiation. 14911 molecules are overexpressed in some tumour cells,  
 CC where they may inappropriately propagate either cell proliferation or  
 CC cell survival signals. The invention provides methods for the diagnosis  
 CC and treatment of cancer, including breast colon, brain and especially

CC lung cancer (claimed), and methods for evaluating the efficacy of  
 CC treatment. 14911 nucleic acids are useful in diagnostic, screening and  
 CC gene therapy methods, for recombinant protein production, in the design  
 CC of probes and primers, as a pharmacogenomics marker, and in the breeding  
 CC of transgenic animals in which a 14911 gene is introduced or disrupted.  
 CC Antisense 14911 and ribozyme molecules are used in a claimed method of  
 CC treating cancer or a cellular proliferation and/or differentiation  
 CC disorder. In addition to cancer, such disorders include those associated  
 CC with bone metabolism, autoimmune diseases, cardiovascular disorders,  
 CC liver disorders, viral diseases, pain and metabolic disorders  
 XX  
 SQ Sequence 1281 BP; 392 A; 277 C; 299 G; 313 T; 0 U; 0 Other;  
 Query Match 82.7%; Score 1228.6; DB 6; Length 1281;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCATGGGAGCGAACACTTCAAGAAACCCACAGATGTTGATGAAATGAAGATGTCACCT 60  
 DB |||||  
 QY 47 CCATGGGAGCGAACACTTCAAGAAACCCACAGATGTTGATGAAATGAAGATGTCACCT 106  
 DB |||||  
 QY 61 TTGACCACTTTGAAATTTTGGAGCAATTTGGGAAAGGCGATTTTGGGAGGTCTGCATTTG 120  
 DB |||||  
 QY 107 TTGACCACTTTGAAATTTTGGAGCAATTTGGGAAAGGCGATTTTGGGAGGTCTGCATTTG 166  
 DB |||||  
 QY 121 TACAGAGAGATGATACCAAGAGATGTCGGCAATGAAGTACATGATTAACAAAGTGGG 180  
 DB |||||  
 QY 167 TACAGAGAGATGATACCAAGAGATGTCGGCAATGAAGTACATGATTAACAAAGTGGG 226  
 DB |||||  
 QY 181 TGGAGCGCAATGAAGTGAAGATGCTTCAAGGAACTCCAGATCATGAGGTCTGGAGC 240  
 DB |||||  
 QY 227 TGGAGCGCAATGAAGTGAAGATGCTTCAAGGAACTCCAGATCATGAGGTCTGGAGC 286  
 DB |||||  
 QY 241 ACCCTTCTCTGTTAAATTTGGGTATTCCTTCCAAGATGAGGAAAGCATGTTTCATGTTGG 300  
 DB |||||  
 QY 287 ACCCTTCTCTGTTAAATTTGGGTATTCCTTCCAAGATGAGGAAAGCATGTTTCATGTTGG 346  
 DB |||||  
 QY 301 TGGACCTCTCTGTTGGTGGAGACCTGCTTATCACTTCAAGAGAACTCCACATGCTCAAGG 360  
 DB |||||  
 QY 347 TGGACCTCTCTGTTGGTGGAGACCTGCTTATCACTTCAAGAGAACTCCAGATCATGAGGTCT 406  
 DB |||||  
 QY 361 AAGAAACAGTGAAGCTCTTCACTGTGTGAGCTGGTTCATGCTGAGTCCCTGAGTACCTTGCAGAAC 420  
 DB |||||  
 QY 407 AAGAAACAGTGAAGCTCTTCACTGTGTGAGCTGGTTCATGCTGAGTCCCTGAGTACCTTGCAGAAC 466  
 DB |||||  
 QY 421 AGCGATCATTCACAGGATATGAAGCTTGACATATTTTACTTTCAGCAACATGCGGACG 480  
 DB |||||  
 QY 467 AGCGATCATTCACAGGATATGAAGCTTGACATATTTTACTTTCAGCAACATGCGGACG 526  
 DB |||||  
 QY 481 TGCATCATCAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTAACACCA 540  
 DB |||||  
 QY 527 TGCATCATCAGATTTCAACATTTGCTGCGATGCTGCCAGGAGATACAGATTAACACCA 586  
 DB |||||  
 QY 541 TGGCTGGCAACCAAGCTTTACATGTCACCTGAGATGTTTTCAGCTTCCAGAAAGAGAGAGCT 600  
 DB |||||  
 QY 587 TGGCTGGCAACCAAGCTTTACATGTCACCTGAGATGTTTTCAGCTTCCAGAAAGAGAGAGCT 646  
 DB |||||  
 QY 601 ATTCCTTTGCTGTTGATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660  
 DB |||||  
 QY 647 ATTCCTTTGCTGTTGATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 706  
 DB |||||  
 QY 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGATACACAGTCTTGAGA 720  
 DB |||||  
 QY 707 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGATACACAGTCTTGAGA 766  
 DB |||||  
 QY 721 CGACTGTTGTAACCTTTCCTGCTGGTTCAGAGAAATGTTGTCATCTTTTAAAGAGC 780  
 DB |||||  
 QY 767 CGACTGTTGTAACCTTTCCTGCTGGTTCAGAGAAATGTTGTCATCTTTTAAAGAGC 826  
 DB |||||  
 QY 781 TACTCGAACCTTAATCCAGCAACCAAGTCTTCTCAGTATCTGATCTCCAGACTTCCCGT 840  
 DB |||||  
 QY 827 TACTCGAACCTTAATCCAGCAACCAAGTCTTCTCAGTATCTGATCTCCAGACTTCCCGT 886  
 DB |||||







Db 361 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCAATGGCCCTGACCTACCTGACAGAACAG 420  
Qy 423 CGCATCAATTCACAGGATATGAAGCTGCAATAATTTTACTTGAAGCAATGGGCACTGG 482  
Db 421 CGCATCAATTCACAGGATATGAAGCTGCAATAATTTTACTTGAAGCAATGGGCACTGG 480  
Qy 483 CACATCACAGATTTCACATTTGCTGGATGCTGCCAGGAGACACAGATTACCAACCATG 542  
Db 481 CACATCACAGATTTCACATTTGCTGGATGCTGCCAGGAGACACAGATTACCAACCATG 540  
Qy 543 GCTGGCAACCAAGCTTACATGCGACCTGAGATGCTTCAGTCCAGAAAAGGAGCAGGCTAT 602  
Db 541 GCTGGCAACCAAGCTTACATGCGACCTGAGATGCTTCAGTCCAGAAAAGGAGCAGGCTAT 600  
Qy 603 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACCGGATATGAATCTGCTGAGAGCCGG 662  
Db 601 TCCTTTGCTGTGACTGGTGGTCCCTGGGAGTGACCGGATATGAATCTGCTGAGAGCCGG 660  
Qy 663 AGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATGTCACACGTTTGAGAGC 722  
Db 661 AGACCGTATCATATTGCTCCAGTACTTCCAGCAAGGAAATGTCACACGTTTGAGAGC 720  
Qy 723 ACTGTGTAACTTACCTCTCTGCTGGTCA CAGGAAATGGTGTCACTTCTTAAAGCTA 782  
Db 721 ACTGTGTAACTTACCTCTCTGCTGGTCA CAGGAAATGGTGTCACTTCTTAAAGCTA 780  
Qy 783 CTGAACTTAATCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCGCTAT 842  
Db 781 CTGAACTTAATCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCGCTAT 840  
Qy 843 ATCAATGATATAAATCGGATGACATTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 902  
Db 841 ATCAATGATATAAATCGGATGACATTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900  
Qy 903 AATAAGGCGAGCTGAATTTGTATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 962  
Db 901 AATAAGGCGAGCTGAATTTGTATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 960  
Qy 963 AAACCTCTACATGAAGAAAAGCTCTGGCAAGAGGAGGAGGATATGAGGAATGC 1022  
Db 961 AAACCTCTACATGAAGAAAAGCTCTGGCAAGAGGAGGAGGATATGAGGAATGC 1020  
Qy 1023 GATTTCTTCAGACATGCTCTTCTTCAAGAGCCTTGACTCTCTGTCAGAGGAGGATTCATA 1082  
Db 1021 GATTTCTTCAGACATGCTCTTCTTCAAGAGCCTTGACTCTCTGTCAGAGGAGGATTCATA 1080  
Qy 1083 ATTTTCAACAGAGAAAAGTAAACAGGACTTTTAA CAAAAGACAA CAAATCTAGCCTTG 1142  
Db 1081 ATTTTCAACAGAGAAAAGTAAACAGGACTTTTAA CAAAAGACAA CAAATCTAGCCTTG 1140  
Qy 1143 GAACAACCAAGACCAAGCTGAGGATGGTCAGAAATCAACCTTGTA 1193  
Db 1141 GAACAACCAAGACCAAGCTGAGGATGGTCAGAAATCAACCTTGTA 1191

## RESULT 7

AD23680  
ID AD23680 standard; DNA; 1675 BP.

AC AD23680;

XX 07-MAR-2002 (first entry)

XX Novel human protein (NHP) kinase full-length ORF and flanking region DNA.

XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
XX gene expression; breast cancer; prostate cancer; nutritional; cosmetic;  
XX medical disorder; mental; biological; physiological; chemotherapeutic;  
XX ds.

OS Homo sapiens.

XX

PN WO200181557-A2.

PD 01-NOV-2001.

XX 24-APR-2001; 2001WO-US013149.

XX 25-APR-2000; 2000US-0199499P.

XX 01-MAY-2000; 2000US-0201227P.

XX (LEXI-) LEXICON GENETICS INC.

XX Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;

XX WPI; 2002-034442/04.

XX New nucleic acid molecules encoding new human proteins, useful in  
PT diagnosis, drug screening, clinical trial monitoring, treatment of  
PT physiological disorders, and cosmetic or nutraceutical applications.

XX Disclosure; Page 44; 44pp; English.

XX The invention relates to novel human protein (NHP) kinases and their  
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as  
CC reagents in assays for screening compounds that can be used as  
CC pharmaceutical reagents useful in the therapeutic treatment of mental,  
CC biological and medical disorders, and also as chemotherapeutic agents  
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is  
CC useful for diagnosis, drug screening, clinical trial monitoring, the  
CC treatment of physiological disorders or diseases, and cosmetic and  
CC nutraceutical applications. NHP DNA is also useful for the identification  
CC of coding sequence and the mapping of a unique gene to a particular  
CC chromosome. NHP DNA is further useful as hybridisation probes for  
CC screening libraries and assessing gene expression patterns, and also for  
CC the detection of mutant NHPs or inappropriately expressed NHPs for  
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present  
CC sequence is novel human protein (NHP) kinase full-length ORF (open  
CC reading frame) and flanking region DNA related to the invention  
XX

SQ Sequence 1675 BP; 469 A; 404 C; 414 G; 388 T; 0 U; 0 Other;

Query Match 78.3%; Score 1162.6; DB 6; Length 1675;

Best Local Similarity 98.8%; Pred. No. 6.7e-312;

Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCATGGGAGCGAACAACCTTCAAGAAAACCAACAGTGTGTGATGAAATGAAGATGCAACT 60

Db 411 CCATGGGAGCGAACAACCTTCAAGAAAACCAACAGTGTGTGATGAAATGAAGATGCAACT 470

Qy 61 TTGACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGAGTGTGGGAGGCTGTGATTG 120

Db 471 TTGACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGAGTGTGGGAGGCTGTGATTG 530

Qy 121 TACAGAGGATGATACCAAGAGATGTGGCAATGATGATGATGATGATGATGATGATGATG 180

Db 531 TACAGAGGATGATACCAAGAGATGTGGCAATGATGATGATGATGATGATGATGATGATG 590

Qy 181 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACTCCAGATCATGCAAGGCTGTGGAGC 240

Db 591 TGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACTCCAGATCATGCAAGGCTGTGGAGC 650

Qy 241 ACCCTTTCTGTTAAATTTTGGTATTTCTTCCAGATGAGGAGACATGTTTCATGTTGG 300

Db 651 ACCCTTTCTGTTAAATTTTGGTATTTCTTCCAGATGAGGAGACATGTTTCATGTTGG 710

Qy 301 TGGACTCTCTGCTGGTGGAGACCTGCGTTATCCTGCAACAGACGTCCTCACTTCAAGG 360

Db 711 TGGACTCTCTGCTGGTGGAGACCTGCGTTATCCTGCAACAGACGTCCTCACTTCAAGG 770

Qy 361 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGCGCTGAGTACCTGCAAGACC 420

Db 771 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTTCATGCGCTGAGTACCTGCAAGACC 830

Qy 421 AGCGCATCATTCACAGGAGATGAAAGCTGACATATTTTACTTTCAGACATGCGGACG 480



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Db 831 AGCGCATATTACAGGATATGAAGCTTGACAAATATTTACTTGACGACATGGCAG 890
Qy 481 TGCACATCAGAGATTTCAACATTTGCTGCGATGCTGCCCAAGGAGACACAGATTAACCA 540
Db 891 TGCACATCAGAGATTTCAACATTTGCTGCGATGCTGCCCAAGGAGACACAGATTAACCA 950
Qy 541 TGGCTGGCACCAGCCTTACATGCGACCTTGAGATGTTGAGTCCAGAAAGGAGCAGGCT 600
Db 951 TGGCTGGCACCAGCCTTACATGCGACCTTGAGATGTTGAGTCCAGAAAGGAGCAGGCT 1010
Qy 601 ATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGCGCATATGAACCTGCTGAGAGCC 660
Db 1011 ATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGCGCATATGAACCTGCTGAGAGCC 1070
Qy 661 GGAGACCGTATCATATTTGCTGCTCAGTACTTCCAGCAAGGAATTTGACACAGTTTGAGA 720
Db 1071 GGAGACCGTATCATATTTGCTGCTCAGTACTTCCAGCAAGGAATTTGACACAGTTTGAGA 1130
Qy 721 CGACTGTTGTAATTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 1131 CGACTGTTGTAATTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1190
Qy 781 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGT 840
Db 1191 TACTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGT 1250
Qy 841 ATATGATGATATAAATCGGATGATGATTTTTCAGAGAGGCTCATTCAGGTTTCATTC 900
Db 1251 ATATGATGATATAAATCGGATGATGATTTTTCAGAGAGGCTCATTCAGGTTTCATTC 1310
Qy 901 CTAATAAGGAGGCTGATTTGATGCTTCTTACCTTTGAACTTCAGGAAATGATTTTGGAGT 960
Db 1311 CTAATAAGGAGGCTGATTTGATGCTTCTTACCTTTGAACTTCAGGAAATGATTTTGGAGT 1370
Qy 961 CCAAACTCTACATAAGAAAAAAGCGCTCTGCGAAAGAGGAGGATATGAGGAAT 1020
Db 1371 CCAAACTCTACATAAGAAAAAAGCGCTCTGCGAAAGAGGAGGATATGAGGAAT 1430
Qy 1021 GCGATTTCTCAGACATGCTTCTTCTCAAGACACCTTGACTCTGCTGCGAAGGAGTTCA 1080
Db 1431 GCGATTTCTCAGACATGCTTCTTCTCAAGACACCTTGACTCTGCTGCGAAGGAGTTCA 1490
Qy 1081 TAATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGACAAACCAATCTAGCT 1140
Db 1491 TAATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGACAAACCAATCTAGCT 1550
Qy 1141 TGGAAACAAACCAAGACCCCAAGTGGAGTGGTGCAGAAATAACA 1185
Db 1551 TGGAAACAAACCAAGACCCCAAGTGGAGTGGTGCAGAAATAACA 1595

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## RESULT 8

AAD23678

ID AAD23678 standard; cDNA; 1224 BP.

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

XX AAD23678;

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WO200181557-A2.

01-NOV-2001.

24-APR-2001; 2001WO-US013149.

25-APR-2000; 2000US-0199499P.

01-MAY-2000; 2000US-0201227P.

(LEXI-) LEXICON GENETICS INC.

Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;

WPI; 2002-034442/04.

P-PSDB; AAE14260.

New nucleic acid molecules encoding new human proteins, useful in

diagnosis, drug screening, clinical trial monitoring, treatment of

physiological disorders, and cosmetic or nutraceutical applications.

Claim 4; Page 41; 44pp; English.

The invention relates to novel human protein (NHP) kinases and their

corresponding cDNA molecules. NHP kinase and its DNA are useful as

reagents in assays for screening compounds that can be used as

pharmaceutical reagents useful in the therapeutic treatment of mental,

biological and medical disorders, and also as chemotherapeutic agents

useful in the treatment of breast cancer and prostate cancer. NHP DNA is

useful for diagnosis, drug screening, clinical trial monitoring, the

treatment of physiological disorders or diseases, and cosmetic and

nutraceutical applications. NHP DNA is also useful for the identification

of coding sequence and the mapping of a unique gene to a particular

chromosome. NHP DNA is further useful as hybridisation probes for

screening libraries and assessing gene expression patterns, and also for

the detection of mutant NHPs or inappropriately expressed NHPs for

disease diagnosis. NHP DNA is also useful in gene therapy. The present

sequence is novel human protein (NHP) kinase cDNA which is similar to

serine/threonine protein kinases, ribosomal protein kinases and cAMP-

dependent kinases cDNA related to the invention

Sequence 1224 BP; 381 A; 263 C; 283 G; 297 T; 0 U; 0 Other;

Query Match

Best Local Similarity 78.2%; Score 1160.6; DB 6; Length 1224;

Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

3 ATGGAGCGAACACATTTCAAGAAAACCCAGTGTGTTGATGAAATGAAGATGTCACATTT 62

1 ATGGAGCGAACACATTTCAAGAAAACCCAGTGTGTTGATGAAATGAAGATGTCACATTT 60

63 GACCACTTTGAAATTTGCGAGCCATTTGGGAAGGCGAGTTTGGGAGGCTGTCATTGTA 122

61 GACCACTTTGAAATTTGCGAGCCATTTGGGAAGGCGAGTTTGGGAGGCTGTCATTGTA 120

123 CAGAAGATGATATCAAGAAAGATGTCGCAATGAAGTACATGAATAAATAAAGTGCCTG 182

121 CAGAAGATGATATCAAGAAAGATGTCGCAATGAAGTACATGAATAAATAAAGTGCCTG 180

183 GAGCGCAATGAAGTGAAGAAATGTCCTTCAAGAAATCCAGATCATGACGGTCTGAGCAC 242

181 GAGCGCAATGAAGTGAAGAAATGTCCTTCAAGAAATCCAGATCATGACGGTCTGAGCAC 240

243 CTTTCTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 302

241 CTTTCTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 300

303 GACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 362

301 GACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

363 GAAACAGTGAAGCTCTTCAATCTGTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 422

Db 361 GAAACAGTGAAGCTCTTCTCTGTAGTGGTCAATGGCCCTGAGCTACCTGCGAAGACCG 420  
 Qy 423 CGCATCATTCACAGGATATGAAGCCCTGACAAATATTTTACTTCAGCAATATGGGCGACGTG 482  
 Db 421 CGCATCATTCACAGGATATGAAGCCCTGACAAATATTTTACTTCAGCAATATGGGCGACGTG 480  
 Qy 483 CACATCAGATTTCAACATGCTGCGATGCTGCCAGGAGACACAGATTACCAACATG 542  
 Db 481 CACATCAGATTTCAACATGCTGCGATGCTGCCAGGAGACACAGATTACCAACATG 540  
 Qy 543 GCTGGCACCAAGCCTTACATGCGACCTGAGATGTTCAAGTCCAGAAAAGGAGCAGCTAT 602  
 Db 541 GCTGGCACCAAGCCTTACATGCGACCTGAGATGTTCAAGTCCAGAAAAGGAGCAGCTAT 600  
 Qy 603 TCCTTTGCTGTGATGCTGGTCCCTGGAGTGCAGGATATGAACTGCTGAGAGCCGG 662  
 Db 601 TCCTTTGCTGTGATGCTGGTCCCTGGAGTGCAGGATATGAACTGCTGAGAGCCGG 660  
 Qy 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGACG 722  
 Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGACG 720  
 Qy 723 ACTGTTGTAACTTACCCCTTCTGCTGCTGACAGGAATGCTCACTTCTTAAAAAGCTA 782  
 Db 721 ACTGTTGTAACTTACCCCTTCTGCTGCTGACAGGAATGCTCACTTCTTAAAAAGCTA 780  
 Qy 783 CTGGAACCTAATCAGACCAACAGATTTCTCAGTATCTGATGTCAGAACTTCCCGTAT 842  
 Db 781 CTGGAACCTAATCAGACCAACAGATTTCTCAGTATCTGATGTCAGAACTTCCCGTAT 840  
 Qy 843 ATGAATCATATAACTCGGATGCAAGTCTTTCAGAAAGGAGGCTCATCCAGGTTTCATTCCT 902  
 Db 841 ATGAATCATATAACTCGGATGCAAGTCTTTCAGAAAGGAGGCTCATCCAGGTTTCATTCCT 900  
 Qy 903 AATAAAGGCGAGCTGAATTTGTGATCTTCACTTTGAACTTCAGGAAATGATTTTGGAGTCC 962  
 Db 901 AATAAAGGCGAGCTGAATTTGTGATCTTCACTTTGAACTTCAGGAAATGATTTTGGAGTCC 960  
 Qy 963 AAACCTCTACATATAGAAAAAAGCGTCTGCAAGAGGAGGATATGAGAAATGC 1022  
 Db 961 AAACCTCTACATATAGAAAAAAGCGTCTGCAAGAGGAGGATATGAGAAATGC 1020  
 Qy 1023 GATTTCTCTCAGACATGTTCTTCTCAAGAGCAGCTTCACTCTGTCAGAGAGGATTCATA 1082  
 Db 1021 GATTTCTCTCAGACATGTTCTTCTCAAGAGCAGCTTCACTCTGTCAGAGAGGATTCATA 1080  
 Qy 1083 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGACAAACCAATCTAGCCTTG 1142  
 Db 1081 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGACAAACCAATCTAGCCTTG 1140  
 Qy 1143 GAACAAACCAAGAGACCAAGGAGGATGAGTGGTTCAGATTAACA 1185  
 Db 1141 GAACAAACCAAGAGACCAAGGAGGATGAGTGGTTCAGATTAACA 1183

RESULT 9

AAS06704  
 ID AAS06704 standard; cDNA; 981 BP.  
 XX AC  
 XX AC  
 XX AC  
 XX AC  
 DT 12-SEP-2001 (first entry)  
 XX  
 XX Polynucleotide sequence encoding human protein kinase #4.  
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;  
 KW metabolic disorder; immune related disease; neurological disorder;  
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
 KW reproductive disorder; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200138503-A2.

31-MAY-2001.  
 22-NOV-2000; 2000WO-US032085.  
 24-NOV-1999; 99US-0167482P.  
 (SUGB-) SUGEN INC.  
 Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
 Planagan P, Clary D;  
 WPI: 2001-343950/36.  
 P-PSDB; AAU03504.  
 Nucleic acids encoding human kinase polypeptides, useful for preventing  
 diagnosing and/or treating e.g. cancer, immune, cardiovascular and  
 neuronal-associated diseases, and microbial infections.  
 Example 1; Fig 1; 433pp; English.  
 AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel  
 protein kinases have been identified as members of the tyrosine or  
 serine/threonine kinase (PTK and STK) families. The polynucleotides  
 encoding protein kinases and the polypeptides may be used in the  
 prevention, diagnosis and treatment of diseases associated with  
 inappropriate kinase expression. For example, they may be used to treat  
 cancers (especially cancers of haematopoietic origin), cardiovascular  
 disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
 immune related diseases (e.g. rheumatoid arthritis), neurological  
 disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
 Parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
 disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
 Additionally, polynucleotides encoding protein kinases may be used for  
 gene therapy and as DNA probes in diagnostic assays. The protein kinase  
 polypeptides may be used as antigens in the production of antibodies  
 against the protein kinases and in assays to identify modulators of  
 protein kinase expression and activity  
 Sequence 981 BP; 294 A; 207 C; 245 G; 235 T; 0 U; 0 Other;  
 Query Match 56.0%; Score 831.2; DB 4; Length 981;  
 Best Local Similarity 90.7%; Pred. No. 5.2e-220;  
 Matches 903; Conservative 0; Mismatches 78; Indels 15; Gaps 1;  
 Qy 3 ATGGGAGCGAACAATCTTCAAGAAACCAACAGTGTGTTGATGAAATGAAGATGCACTTT 62  
 Db 1 ATGGGAGCGAACAATCTTCAAGAAACCAACAGTGTGTTGATGAAATGAAGATGCACTTT 60  
 Qy 63 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGAGTGTGTTGGGAGGTCTGCAATTGTA 122  
 Db 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGAGTGTGTTGGGAGGTCTGCAATTGTA 120  
 Qy 123 CAGAAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGATGATGAAACAAAGTGGTG 182  
 Db 121 CAGAAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGATGATGAAACAAAGTGGTG 180  
 Qy 183 GAGCGCAATGAGTGAAGATGCTTCAAGGAACTCCAGATCATGAGGCTCTGGAGCAC 242  
 Db 181 GAGCGCAATGAGTGAAGATGCTTCAAGGAACTCCAGATCATGAGGCTCTGGAGCAC 240  
 Qy 243 CCTTCTCTGTTAATTTTGTGTTATCTTCCAGATGAGGAGACATGTTTCATGGTGGTG 302  
 Db 241 CCTTCTCTGTTAATTTTGTGTTATCTTCCAGATGAGGAGACATGTTTCATGGTGGTG 300  
 Qy 303 GACCTCTCTGCTGGTGGAGACCTGCTTATCACCTGCAACAGAACTGTCATCTTCAAGGAA 362  
 Db 301 GACCTCTCTGCTGGTGGAGACCTGCTTATCACCTGCAACAGAACTGTCATCTTCAAGGAA 360  
 Qy 363 GAAACAGTGAAGCTCTTCTCTGAGTGGTGTGATGCTGCTGAGTACCTGACAGAACAG 422  
 Db 361 GAAACAGTGAAGCTCTTCTCTGAGTGGTGTGATGCTGCTGAGTACCTGACAGAACAG 420



Db 181 TGGTCCCTGGAGTGCAGGATATGAACTCTGAGAGCGCGAGCCGTATCATATTCGC 240  
 Qy 681 TCAGTACTTCCAGCAGGAAATGTACACACGTTTGAGACGACTGTGTAACTTACCCCT 740  
 Db 241 TCCAGTACTTCCAGCAGGAAATGTACACACGTTTGAGACGACTGTGTAACTTACCCCT 300  
 Qy 741 TGTGCTGGTGCAGGAAATGTGTCTCTTTAAAGCTACTCGAACCTTAATCCAGAC 800  
 Db 301 TGTGCTGGTGCAGGAAATGTGTCTCTTTAAAGCTACTCGAACCTTAATCCAGAC 360  
 Qy 801 CAAGGATTTCTAGTATCTGATGTCAGAACTTCCGCTATATGATGATATATAAATGG 860  
 Db 361 CAAGGATTTCTAGTATCTGATGTCAGAACTTCCGCTATATGATGATATATAAATGG 420  
 Qy 861 GATGAGTCTTTCAGAGAGGCTCATTTCCAGGTTTCAATCTTAATAAGGCGGCTGAAT 920  
 Db 421 GATGAGTCTTTCAGAGAGGCTCATTTCCAGGTTTCAATCTTAATAAGGCGGCTGAAT 480  
 Qy 921 TGTGATCTTACTTGAACCTTGAGAAATGATTTGGAGTCCAAACCTCTACATAGAAA 980  
 Db 481 TGTGATCTTACTTGAACCTTGAGAAATGATTTGGAGTCCAAACCTCTACATAGAAA 540  
 Qy 981 AAAAAAGCTCTGGCAAGAGGAGAGATATGAGGAAATGCGAATCTTCTCAGACATGT 1040  
 Db 541 AAAAAAGCTCTGGCAAGAGGAGAGATATGAGGAAATGCGAATCTTCTCAGACATGT 600  
 Qy 1041 CTTCTTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTCATAATTTTCAACAGAGAAAA 1100  
 Db 601 CTTCTTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTCATAATTTTCAACAGAGAAAA 660  
 Qy 1101 GTAAACAGGACTTTA 1116  
 Db 661 GTAAACAGGACTTGA 676

RESULT 11

AAD23677  
 ID AAD23677 standard; cDNA; 711 BP.  
 AC AAD23677;  
 XX AAD23677;  
 DT 07-MAR-2002 (first entry)  
 DE Novel human protein (NHP) kinase cDNA #2.  
 XX Novel human protein (NHP) kinase cDNA #2.  
 KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
 KW gene expression; breast cancer; prostate cancer; nutritional; cosmetic;  
 KW medical disorder; mental; biological; physiological; chemotherapeutic;  
 KW ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 1..711  
 XX /\*tag= a  
 XX /product= "Novel human protein (NHP) kinase"  
 FT  
 FT  
 FT  
 XX WO200181557-A2.  
 XX 01-NOV-2001.  
 XX 24-APR-2001; 2001WO-US013149.  
 XX 25-APR-2000; 2000US-0199499P.  
 XX 01-MAY-2000; 2000US-0201227P.  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX Hu Y, Nepomichy B, Wang X, Donoho G, Scoville J, Walke DW;  
 XX WPI; 2002-034442/04.  
 DR P-PSDB; AAE14259.

XX New nucleic acid molecules encoding new human proteins, useful in  
 PT diagnosis, drug screening, clinical trial monitoring, treatment of  
 PT physiological disorders, and cosmetic or nutraceutical applications.  
 XX Disclosure; Page 40; 44pp; English.  
 XX The invention relates to novel human protein (NHP) kinases and their  
 CC corresponding cDNA molecules. NHP kinase and its DNA are useful as  
 CC reagents in assays for screening compounds that can be used as  
 CC pharmaceutical reagents useful in the therapeutic treatment of mental,  
 CC biological and medical disorders, and also as chemotherapeutic agents  
 CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is  
 CC useful for diagnosis, drug screening, clinical trial monitoring, the  
 CC treatment of physiological disorders of diseases, and cosmetic and  
 CC nutraceutical applications. NHP DNA is also useful for the identification  
 CC of coding sequence and the mapping of a unique gene to a particular  
 CC chromosome. NHP DNA is further useful as hybridisation probes for  
 CC screening libraries and assessing gene expression patterns, and also for  
 CC the detection of mutant NHPs or inappropriately expressed NHPs for  
 CC disease diagnosis. NHP DNA is also useful in gene therapy. The present  
 CC sequence is novel human protein (NHP) kinase cDNA which is similar to  
 CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-  
 CC dependent kinases cDNA related to the invention  
 XX  
 SQ Sequence 711 BP; 199 A; 153 C; 181 G; 178 T; 0 U; 0 Other;  
 Query Match 44.2%; Score 656.2; DB 6; Length 711;  
 Best Local Similarity 99.5%; Pred. No. 1.7e-171;  
 Matches 658; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 3 ATGGGAGCGACACTTCAAGAAACCAACCAAGTGTGTTGATGAAATCAAGATGTCAACTTT 62  
 Db 1 ATGGGAGCGACACTTCAAGAAACCAACCAAGTGTGTTGATGAAATCAAGATGTCAACTTT 60  
 Qy 63 GACCACTTTCAAAATTTTGGAGCCATTTGGGAAGGCGAGTTTGGGAGGTTCTGCATGTGA 122  
 Db 61 GACCACTTTGAAATTTTGGAGCCATTTGGGAAGGCGAGTTTGGGAGGTTCTGCATGTGA 120  
 Qy 123 CAGAAGATGATACCAAGAGATGTGCGCAATGAGTACATGATTAACAACAAAGTGGTG 182  
 Db 121 CAGAAGATGATACCAAGAGATGTGAGCAATGAGTACATGATTAACAACAAAGTGGTG 180  
 Qy 183 GAGCGCAATGAAGTGAAGATGTTTCAAGGAACTCCAGATCATGAGGTTCTGGAGCAC 242  
 Db 181 GAGCGCAATGAAGTGAAGATGTTTCAAGGAACTCCAGATCATGAGGTTCTGGAGCAC 240  
 Qy 243 CTTTCTCTGTTAAATTTTGGTATTCTTCCAAAGATGAGGAACATGTTTCATGTTGGTG 302  
 Db 241 CTTTCTCTGTTAAATTTTGGTATTCTTCCAAAGATGAGGAACATGTTTCATGTTGGTG 300  
 Qy 303 GACCTCTCTGGTGGAGACCTGCTTATCAGCTGCACAGAACGTTCCACTTCAAGGAA 362  
 Db 301 GACCTCTCTGGTGGAGACCTGCTTATCAGCTGCACAGAACGTTCCACTTCAAGGAA 360  
 Qy 363 GAAACAGTGAAGCTCTTCTCTGAGCTGGTCAATGCGCTTACCTGAGAACCCAG 422  
 Db 361 GAAACAGTGAAGCTCTTCTCTGAGCTGGTCAATGCGCTTACCTGAGAACCCAG 420  
 Qy 423 CGCATCATTCACAGGATATGAAGCTGCAATATTTTACTTGACGAACTGGGACGCTG 482  
 Db 421 CGCATCATTCACAGGATATGAAGCTGCAATATTTTACTTGACGAACTGGGACGCTG 480  
 Qy 483 CACATCACAGATTTCAACATTTGCTGGATGCTGCCAGGAGACACAGATTTACCAACATG 542  
 Db 481 CACATCACAGATTTCAACATTTGCTGGATGCTGCCAGGAGACACAGATTTACCAACATG 540  
 Qy 543 GCTGGCACCAAGCTTACATGGCACTGAGATGTTTACGCTCCAGAAAGAGGACAGGCTAT 602  
 Db 541 GCTGGCACCAAGCTTACATGGCACTGAGATGTTTACGCTCCAGAAAGAGGACAGGCTAT 600  
 Qy 603 TCCTTTGCTGTTGAGCTGGTGGTCCCTGGAGTGAAGGCTATGAGTCTGAGAGGCGGG 662

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(HYSB-) HYSEQ INC.

Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
Xue AJ, Yang Y, Wehrman T, Dmanac RT;

WPI; 2002-426278/45.

N-PSDB; ABP43807.

New polypeptides and their encoded proteins, useful as nutritional  
sources or supplements, or in gene therapy, particularly for treating  
wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
inflammation.

Claim 1; SEQ ID # 264; 357pp + Sequence Listing; English.

The invention relates to 446 newly isolated polynucleotide sequences. The  
activity of polynucleotides of the invention may be described as:  
vulnerary, neuroprotective, immunomodulator, cytostatic and anti-  
inflammatory. Compositions comprising nucleic acids of the invention are  
useful for treating a mammalian subject, or as nutritional sources or  
supplements. These are useful in gene therapy, particularly for treating  
wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
inflammation. The nucleic acids and polypeptides are also useful in  
diagnostic and research methods. The sequences given in records ABQ6788-  
ABQ61233 represent polynucleotides of the invention. NOTE: The sequence  
data for this patent did not form part of the printed specification, but  
was obtained in electronic format directly from WIPO at  
ftp.wipo.int/pub/publicated\_sequences

Sequence 1587 BP; 414 A; 421 C; 425 G; 327 T; 0 U; 0 Other;

Query Match 36.4%; Score 540.8; DB 6; Length 1587;

Best Local Similarity 69.1%; Pred. No. 2.8e-139;

Matches 772; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

PA	XX	541	GCTGCAACCAAGCCCTACATGGCTCCAGAGTATTCAGAGGTGTATCATGACACAGAGCCCC	600
PI	XX	597	GGCTATTCCTTGTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGA	656
PI	XX	601	GGATCTCGTACCTGTGACTGGTGGTCCCTGGGATCATCAGACCTATGAGCTGCTGGCG	660
DR	XX	657	GGCCGGAGACCGATATATTCGCTCCAGTATTCCTCAGACAGGAAATGTACACAGTTT	716
PT	XX	661	GGCTGGAGCCGATACGAATCCACTCGGTTCAGGCCCATCGATGAATCTCAACATGTT	720
PT	XX	717	GAGACGACTGTTGTAACTTACCTTCTGCTGCTGCACAGGAATGTGTCACTTCTTAAA	776
PT	XX	721	AAGGTGGAGCGGTCCACTACTCTCCAGTGTGCAAGGGATGTTGGCCCTGCTGAGG	780
PS	XX	777	AAGCTTACTCGAACCCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTC	836
CC	XX	781	AAGCTTCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCTTCATGACATACAGAGCGTG	840
CC	XX	837	CCGTATATGATGATATATACTGGGATGAGTTTTCAGAGAGGCTCATTCAGGTTTC	896
CC	XX	841	CCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAGGCACTGATGCCCGCTTT	900
CC	XX	897	ATTCCTAATAAGGCGAGCTGAATGTGATCTCTACCTTGAACCTTGAAGAAATGATTTG	956
CC	XX	901	GTGCCCAATAAAGGAGGTGAACTGCGATCCCATTTGACCTTGAAGAGATGATTTCTA	960
CC	XX	957	GAGTCCAAACCTCTACATAAGAAAAAAGCGCTCTGGCAAGAA---GGAGAGGATATG	1013
CC	XX	961	GAATCCAGCCACTTCACAAAAAAGAGGATTTGGCAAGAACAGATCCAGGAGTGC	1020
QY	XX	1014	AGAAATGCGATCTTCTCAGACATGTCTTTCAGAGCAGCTTGTGACTCTGTCCAGAG	1073
DB	XX	1021	ACAAAGGACAGCTGCCCGCTGAATGAGACACCTGCGACACTGTTTGGAGACTGTCCGGGAG	1080
QY	XX	1074	GAGTTCATATTTTCAACAGAGAAAAAGTAAACAGGGA	1111
DB	XX	1081	GAATTCATCATATTTCAACAGAGAAAGCTCAGGAGGCA	1118
RESULT 14				
AAFA4625				
ID	AAFA4625	standard; cDNA; 3224 BP.		
XX	AAFA4625;			
AC	AAFA4625;			
XX	27-MAR-2001 (first entry)			
DT	27-MAR-2001			
XX	Novel protein kinase cDNA, SEQ ID NO: 4.			
DE	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
XX	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
KW	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
KW	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
KW	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
KW	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
KW	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
KW	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
KW	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;			
OS	Homo sapiens.			
XX	WO200073469-A2.			
PN	07-DEC-2000.			
XX	26-MAY-2000; 2000WO-US014842.			
XX	28-MAY-1999; 99US-0136503P.			
XX	(SUGB-) SUGEN INC.			
XX	Plowman GD, Martinez R, Whyte D, Sudrean S;			
PI	WPI; 2001-032161/04.			
XX	P-PSDB; AAB65600.			
DR				







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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:03:31 ; Search time 4048 Seconds  
(without alignments)  
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Title: US-10-667-442-1  
Perfect score: 1485  
Sequence: 1 ccattggagcgaacacttca.....taaaaaaaaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1485	100.0	1485	6	AR265353 Sequence
2	1485	100.0	1485	6	AR432044 Sequence
3	1228.6	82.0	1281	6	AX320934 Sequence
4	1188.2	80.0	1594	6	AX207388 Sequence
5	1188.2	80.0	1594	6	AX766348 Sequence
6	1188.2	80.0	1594	6	AX766348 Sequence
7	1186.2	79.9	1191	6	AX393903 Sequence
8	1184.6	79.8	1191	6	AX303185 Sequence
9	1162.6	78.3	1675	6	AX320936 Sequence
10	1162.6	78.3	1675	6	AX393904 Sequence
11	1162.6	78.3	1675	6	AX303187 Sequence
12	1160.6	78.2	1224	6	AX393902 Sequence
13	1029.4	69.3	2063	6	AX303183 Sequence
14	1029.4	69.3	2063	6	AX833107 Sequence
15	831.2	56.0	981	6	AX094580 Homo sapi
16	792.4	53.4	4973	10	AX166513 Sequence
17	656.2	44.2	711	6	BC055002 Mus muscu
18	656.2	44.2	711	6	AR393901 Sequence
19	655.2	44.1	678	6	AX303181 Sequence
20	655.2	44.1	678	6	AX393900 Sequence
21	556.8	37.5	3367	10	AX303179 Sequence
22	556.8	37.5	3367	10	BC058412 Mus muscu
23	556.8	37.5	3367	10	BC052404 Mus muscu
24	553.6	37.3	3449	10	BC056396 Mus muscu
25	540.8	36.4	3224	6	AX250840 Mus muscu
26	540.8	36.4	3224	6	AX056360 Sequence
27	539.2	36.3	3236	9	AX056360 Sequence
28	516.4	34.8	3244	6	AX098866 Homo sapi
29	516.4	34.8	3244	6	AX376504 Sequence
30	494.4	33.3	2184	10	AX358353 Homo sapi
31	494.4	33.3	2201	10	BC026457 Mus muscu
32	481.6	32.4	1257	6	AB041542 Mus muscu
33	481.6	32.4	1826	6	AR411704 Sequence
34	481.6	32.4	2143	9	AR411703 Sequence
35	480	32.3	1487	6	AY098866 Homo sapi
36	480	32.3	1858	9	AX504245 Sequence
37	476.2	32.1	1787	6	BC015792 Homo sapi
38	469.6	31.6	827	9	AX056359 Sequence
39	468.4	31.5	2028	9	BC021666 Homo sapi
40	466.8	31.4	1864	6	BC045760 Homo sapi
41	462	31.1	1591	6	AX642304 Sequence
42	458.2	30.9	1640	6	AX768900 Sequence
43	457.4	30.8	2038	9	AX179651 Sequence
44	445.4	30.0	1868	9	AB056389 Macaca fa
45	441.8	29.8	2182	6	AK057849 Homo sapi
					AX364903 Sequence

ALIGNMENTS

RESULT 1	AR265353	Sequence 1 from patent US 6492155.	1485 bp	DNA	linear	PAT 10-APR-2003
LOCUS	AR265353					
DEFINITION	Sequence 1 from patent US 6492155.					
ACCESSION	AR265353					
VERSION	AR265353.1	GI:29693863				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1485)					
AUTHORS	Ye,J., Yan,C., Di Francesco,V. and Beasley,E.M.					
TITLE	Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof					
JOURNAL	Patent: US 6492155-A 1 10-DEC-2002;					

FEATURES  
source Location/Qualifiers  
1.1485  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1485; DB 6; Length 1485;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGGAGCGAACACCTTCAAGAAACCCACAGTGTGATGAAATGAAGATGTCAACT 60  
DB 1 CCATGGAGCGAACACCTTCAAGAAACCCACAGTGTGATGAAATGAAGATGTCAACT 60

QY 61 TTGACCACTTTGAAATTTTGGAGCCCAATGGGAAAGCAGTTTGGGAGGCTTCGATTG 120  
DB 61 TTGACCACTTTGAAATTTTGGAGCCCAATGGGAAAGCAGTTTGGGAGGCTTCGATTG 120

QY 121 TACAGAGATGATACCAAGAGATGCGCAATGAAGTACATGAATGAATGAAGTGGC 180  
DB 121 TACAGAGATGATACCAAGAGATGCGCAATGAAGTACATGAATGAATGAAGTGGC 180

QY 181 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGCAAGGCTCGAGC 240  
DB 181 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGCAAGGCTCGAGC 240

QY 241 ACCCTTTCTGGTTAAATTTGGGTAATTCCTTCCAGATGAGGAAAGACATGTTCAATGGTGG 300  
DB 241 ACCCTTTCTGGTTAAATTTGGGTAATTCCTTCCAGATGAGGAAAGACATGTTCAATGGTGG 300

QY 301 TGGAGCTTCTGGTGGAGACCTGCTTATCACTGCAACAGAGCTCCACTTCAAGG 360  
DB 301 TGGAGCTTCTGGTGGAGACCTGCTTATCACTGCAACAGAGCTCCACTTCAAGG 360

QY 361 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTCACTGGCCCTGGACTACTCGAGAAC 420  
DB 361 AAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTCACTGGCCCTGGACTACTCGAGAAC 420

QY 421 AGCGCATCATTCAGGATATGAAGCTGACAAATATTTACTTGAAGAAAGAGAGAGCT 480  
DB 421 AGCGCATCATTCAGGATATGAAGCTGACAAATATTTACTTGAAGAAAGAGAGAGCT 480

QY 481 TGACATCACAGATTTCAACATGCTGCGATGCTGCCAGGAGACACAGATTAACACCA 540  
DB 481 TGACATCACAGATTTCAACATGCTGCGATGCTGCCAGGAGACACAGATTAACACCA 540

QY 541 TGGCTGGCACCACAGCTTACATGGCACCTGAGATGTTTCACTCCAGAAAGAGAGAGCT 600  
DB 541 TGGCTGGCACCACAGCTTACATGGCACCTGAGATGTTTCACTCCAGAAAGAGAGAGCT 600

QY 601 ATTCTTTGCTGTGATGCTGGTGGTCCCTGGAGTGAAGGATATGAAGTGTGAGAGCC 660  
DB 601 ATTCTTTGCTGTGATGCTGGTGGTCCCTGGAGTGAAGGATATGAAGTGTGAGAGCC 660

QY 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACAGTTTCAGA 720  
DB 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACAGTTTCAGA 720

QY 721 CGACTGTGTAACTTACCTTCTGCTGGTCCAGGAAATGGTGTCACTTCTTAAAGAGC 780  
DB 721 CGACTGTGTAACTTACCTTCTGCTGGTCCAGGAAATGGTGTCACTTCTTAAAGAGC 780

QY 781 TACTCGACCTTAATCCAGACCAAGATTTCTCAGTATCTGATGTCAGACCTTCGGT 840  
DB 781 TACTCGACCTTAATCCAGACCAAGATTTCTCAGTATCTGATGTCAGACCTTCGGT 840

QY 841 ATATGAATGATATAAATCTGGGATGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTC 900  
DB 841 ATATGAATGATATAAATCTGGGATGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTC 900

QY 901 CTAATAAGGAGGCTGAATGATGATCTTCACTTTGAACTTGAAGAAATGATTTGGAGT 960  
DB 901 CTAATAAGGAGGCTGAATGATGATCTTCACTTTGAACTTGAAGAAATGATTTGGAGT 960

QY 961 CCAAACTCTCATAGAAAAAAGCGCTCTGGCAAAGAGAGGATATGAGGAAAT 1020  
DB 961 CCAAACTCTCATAGAAAAAAGCGCTCTGGCAAAGAGAGGATATGAGGAAAT 1020

QY 1021 GCGATTTCTCTCAGACATGCTCTTCAAGAGCACCTTCACTCTGCTCCAGAGGAGTTCA 1080  
DB 1021 GCGATTTCTCTCAGACATGCTCTTCAAGAGCACCTTCACTCTGCTCCAGAGGAGTTCA 1080

QY 1081 TAAATTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAATCTAGCCT 1140  
DB 1081 TAAATTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAATCTAGCCT 1140

QY 1141 TGGACAAACCAAGAGCCCAAGGTGAGATGCTCAGATTAACAATCTTGTAAAGGCTTC 1200  
DB 1141 TGGACAAACCAAGAGCCCAAGGTGAGATGCTCAGATTAACAATCTTGTAAAGGCTTC 1200

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DB 1201 ATGTCTTCTTCTTGGGACCAATCTCATGCCAGAACTTTCTAAATTAATATGTCAGAAAG 1260

QY 1261 CTGACAGTAGCTCTCTCCACTCCACACCATGACTTAGAAAAATGTAATGATATATTT 1320  
DB 1261 CTGACAGTAGCTCTCTCCACTCCACACCATGACTTAGAAAAATGTAATGATATATTT 1320

QY 1321 CAAAAAGGAGCAGCAACACAGTGAAGGCTCTGGGCTGAGCTCTGGAAAGTCAATTC 1380  
DB 1321 CAAAAAGGAGCAGCAACACAGTGAAGGCTCTGGGCTGAGCTCTGGAAAGTCAATTC 1380

QY 1381 ACATCAATCACTGTGTGATCTAGAGCAAGTCACTTAGCCACTTTCTGTGCTTTACTTTA 1440  
DB 1381 ACATCAATCACTGTGTGATCTAGAGCAAGTCACTTAGCCACTTTCTGTGCTTTACTTTA 1440

QY 1441 TTTATCTAAATGAGAGGTTTATCTAAAAAAAAGGAAAAA 1485  
DB 1441 TTTATCTAAATGAGAGGTTTATCTAAAAAAAAGGAAAAA 1485

RESULT 2  
AR432044  
LOCUS 1485 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1 from patent US 6653117.  
ACCESSION AR432044  
VERSION AR432044.1 GI:40194241  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1485)  
AUTHORS Ye, J., Yan, C., Di Francesco, V. and Beasley, E.M.  
TITLE Isolated human kinase proteins  
JOURNAL Patent: US 6653117-A 1 25-NOV-2003;  
FEATURES Location/Qualifiers  
Source 1.1485  
/organism="unknown"  
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ORIGIN

Query Match 100.0%; Score 1485; DB 6; Length 1485;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 TGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACTCCAGATCATGCAAGGCTCGAGC 240  
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1247 ATGTCTTCTTCTTGGGCAATCTCATGCTGAGGAT 1281

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LOCUS

AX207388 1594 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 1 from Patent WO0155356.  
ACCESSION AX207388  
VERSION AX207388.1 GI:15395198  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Plowman,G., Whyte,D., Manning,G., Sudarsanam,S. and Martinez,R.  
TITLE Human protein kinases and protein kinase-like enzymes  
JOURNAL Patent: WO 0155356-A 1 02-AUG-2001;  
Sugen, Inc. (US)  
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Best Local Similarity 99.7%; Pred. No. 2.7e-286;  
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1182	Db	TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGTATGTCGAGAACTTCCCGT	1241
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
ORIGIN
Query Match
Best Local Similarity
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LOCUS
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
FEATURES
SOURCE
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Query Match
Best Local Similarity
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Pred. No. 8.4e-286;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hu, Y., Nepomichy, B., Wang, X., Donoho, G., Scoville, J. and
Walke, D.W.
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Patent: WO 0181557-A 10 01-NOV-2001;
Lexicon Genetics Incorporated (US)
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DEFINITION Sequence 12 from patent US 6617147.
ACCESSION AR393904
VERSION AR393904.1 GI:40121081
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1675)
AUTHORS Hu, Y., Nepomichy, B., Wang, X. and Donoho, G.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6617147-A 12 09-SEP-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 98.8%; Pred. No. 6.9e-280;
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 61 TTGACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAGGCTCTGCATTG 120
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QY 121 TACGAAGATGATACCAAGAGATGTCGCGCAATGAAGTACATGATTAACAAAGATGCG 180
Db 531 TACGAAGATGATACCAAGAGATGTCGCGCAATGAAGTACATGATTAACAAAGATGCG 590
QY 181 TGGAGCGCAATGAAGTGAAGATGCTTCAAGGAACTCCAGATCATGAGGCTCTGGAGC 240
Db 591 TGGAGCGCAATGAAGTGAAGATGCTTCAAGGAACTCCAGATCATGAGGCTCTGGAGC 650
QY 241 ACCCTTTCTGTTAATTTGGTATTCCTTCCAGATGAGGAGACATGTTCAATGGTGG 300
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QY 301 TGGACCTCTGCTGGGTGGAGACCTGCGTTATCACTGCAACAGAACGTCCACTTCAAGG 360
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QY 361 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGGCCCTTGGACTACTTCCAGAAC 420
Db 771 AAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGGCCCTTGGACTACTTCCAGAAC 830
QY 421 AGCGCATCAATCAAGGGATATGAAGCCTTGAACAATATTTTACCTTGAACGAATGGGACG 480
Db 831 AGCGCATCAATCAAGGGATATGAAGCCTTGAACAATATTTTACCTTGAACGAATGGGACG 890
QY 481 TGCACATCAGAGTTTCAACATTTGTCGATCTGCGGATCTGCCAGGGGAGACACAGATTACCA 540
Db 891 TGCACATCAGAGTTTCAACATTTGTCGATCTGCGGATCTGCCAGGGGAGACACAGATTACCA 950
QY 541 TGGCTGGCACCAAGCCTTACATGGCACCTTGAGATGTTTCAAGTCCAGAAAGAGAGAGGCT 600
Db 951 TGGCTGGCACCAAGCCTTACATGGCACCTTGAGATGTTTCAAGTCCAGAAAGAGAGAGGCT 1010
QY 601 ATTCTTTTGTGTTGATCTGGTCCCTGGGAGTGAACGATATGATGATGCTGAGAGGCC 660
Db 1011 ATTCTTTTGTGTTGATCTGGTCCCTGGGAGTGAACGATATGATGATGCTGAGAGGCC 1070
QY 661 GGAGACGCTATCATATTTCCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGA 720
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QY 841 ATATGATGATATAAAGCTGGGATGTCAGTTTTCAGAGAGGCTCATTCAGAGTTTCATTC 900
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QY 961 CCAAACTCTACATAGAAAAAAGGCTCTGCAAGAGAGGAGGATATGAGGAAAT 1020
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## RESULT 10

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DEFINITION Sequence 12 from Patent WO0181557.
ACCESSION AR303187
VERSION AR303187.1 GI:17383669
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE  
1  
AUTHORS  
Hu, Y., Nepomnichy, B., Wang, X., Donoho, G., Scoville, J. and  
Walke, D.W.  
TITLE  
Human kinase proteins and polynucleotides encoding the same  
JOURNAL  
Patent: WO 0181557-A 12 01-NOV-2001;  
Lexicon Genetics Incorporated (US)  
FEATURES  
Location/Qualifiers  
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Query Match  
Best Local Similarity 78.3%; Score 1162.6; DB 6; Length 1675;  
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Qy 1 CCATGGGAGGCAACATTTCAAGAAACCCACAGTGTGATGAAATGAAGATGCAACT 60  
Db 411 CCATGGGAGGCAACATTTCAAGAAACCCACAGTGTGATGAAATGAAGATGCAACT 470  
Qy 61 TTGACCACTTTGAATTTTGGAGGCAATGGGAAGGCAAGTTTGGGGAGGTCTGCATTG 120  
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Qy 241 ACCCTTCTGTTGTAATTTGGTATATCTTCCAGATGAGGAAGACATGTTCATGTGTG 300  
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Qy 421 AGCGCATCATTCACAGGATATGAAGCTGACATATTTTACTTGAAGAACATGGGCACG 480  
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Qy 481 TGCACATCACAGATTTCAACATTTGCTGGATGCTGCCAGGAGACACAGATTACCACCA 540  
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DEFINITION Sequence 8 from patent US 6617147.  
ACCESSION AR393902  
VERSION AR393902.1 GI:40121077  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1224)  
AUTHORS Hu, Y., Nepomnichy, B., Wang, X. and Donoho, G.  
TITLE Human kinase proteins and polynucleotides encoding the same  
JOURNAL Patent: US 6617147-A 8 09-SEP-2003;  
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Best Local Similarity 98.8%; Pred. No. 2.2e-279;  
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REFERENCE 2 (bases 1 to 2063)  
 AUTHORS Isogai, T. and Yamamoto, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

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 VERSION AX166513.1 GI:14546858  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,  
 Flanagan, P. and Clary, D.S.  
 TITLE Novel human protein kinases and protein kinase-like enzymes  
 JOURNAL Patent: WO 0138503-A 4 31-MAY-2001;  
 Sugen, Inc. (US)

FEATURES  
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 Best Local Similarity 90.7%; Pred. No. 6.1e-197;  
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QY 3 ATGGGAGCGAACACATCTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 62  
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 QY 63 GACCACTTTGAAATTTTGGAGCCATTTGGAAAGCGAGTTTGGGGAGGCTCTGCATTGTA 122  
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 QY 183 GAGCGCAATGAAGTGAAGAAATCTTTCAGAGGAACCTCCAGATCATGACAGGCTCTGGAGCAC 242  
 DB 181 GAGCGCAATGAAGTGAAGAAATCTTTCAGAGGAACCTCCAGATCATGACAGGCTCTGGAGCAC 240





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:47:04 ; Search time 44 Seconds  
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2839.664 Million cell updates/sec

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Perfect score: 2104

Sequence: 1 MGANTSRRKPPFVDENDVNF.....NLAEQTKPQGGDQNNNL 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- SPTREMBL 25:\*\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
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15: sp\_rviro:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1726	82.0	368	11 Q7TPQ4	Q7TPQ4 mus musculus
3	1438.5	68.4	414	11 Q7TMD3	Q7TMD3 mus musculus
4	1437.5	68.3	414	11 Q9JXK8	Q9JXK8 mus musculus
5	1434.5	68.2	414	11 Q8C4E0	Q8C4E0 mus musculus
6	1425.5	67.8	414	4 Q9NY57	Q9NY57 homo sapien
7	1421.5	67.6	414	4 Q8IY14	Q8IY14 homo sapien
8	1324	62.9	486	4 Q86UX6	Q86UX6 homo sapien
9	1317.5	62.6	488	11 Q9JUG4	Q9JUG4 mus musculus
10	1317.5	62.6	488	11 Q8QV4	Q8QV4 mus musculus
11	1137.5	54.1	369	4 Q86BA3	Q86BA3 homo sapien
12	1137.5	54.1	369	4 Q86UE1	Q86UE1 homo sapien
13	1122.5	53.4	368	6 Q86GT4	Q86GT4 macaca fasc
14	843.5	40.1	379	5 Q21483	Q21483 caenorhabdi
15	822	39.1	166	4 Q8WU08	Q8WU08 homo sapien
16	711.5	33.8	700	5 Q9VN23	Q9VN23 drosophila

17	675	32.1	367	3	Q96WJ8	Q96WJ8 blumeria gr
18	548.5	26.1	735	5	Q8I4W3	Q8I4W3 plasmodium
19	521	24.8	480	10	Q43380	Q43380 avena sativ
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23	513.5	24.4	352	5	Q25115	Q25115 hemientrot
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25	512	24.3	462	5	Q97116	Q97116 amblyomma a
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27	508	24.1	371	5	Q97114	Q97114 amblyomma a
28	507.5	24.1	530	3	Q42793	Q42793 colletoctric
29	507.5	24.1	919	3	Q8N1K8	Q8N1K8 emricella
30	507	24.1	352	5	Q16957	Q16957 alysia cal
31	506.5	24.1	772	5	Q18846	Q18846 caenorhabdi
32	506.5	24.1	917	3	Q9HGS0	Q9HGS0 botrytis ci
33	504.5	24.0	536	3	Q9P466	Q9P466 neurospora
34	502.5	23.9	502	3	Q8J129	Q8J129 aspergillus
35	501.5	23.8	726	4	Q7Z327	Q7Z327 homo sapien
36	501.5	23.8	726	6	Q7YQL2	Q7YQL2 pan troglod
37	501.5	23.8	726	6	Q7YQL1	Q7YQL1 pongo pygma
38	501.5	23.8	758	6	Q9BR29	Q9BR29 macaca fasc
39	501	23.8	360	5	Q16933	Q16933 ancylostoma
40	500.5	23.8	351	13	Q90WN3	Q90WN3 xenopus lae
41	500.5	23.8	490	3	Q96UM3	Q96UM3 aspergillus
42	500.5	23.8	733	4	Q96J38	Q96J38 homo sapien
43	499.5	23.7	587	4	Q8WU06	Q8WU06 homo sapien
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ALIGNMENTS

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DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Similar to serine threonine kinase 32 homolog.			
GN	A930015B13RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
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[1]				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The PANTOM Consortium			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RL	Nature 420:563-573(2002)."			
DR	EMBL; AK036266; BAC29366.1; -			
DR	EMBL; AK042599; BAC31302.1; -			
DR	EMBL; AK044474; BAC31941.1; -			
DR	MGI; MGI:2442403; A930015B13RIK.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR008271; Ser_thr_kinase.			
DR	InterPro; IPR001245; Tyr_kinase.			
DR	Pfam; PF00069; pkinase; 1.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00220; S_TKC; 1.			
DR	SMART; SM00219; Tyrkc; 1.			

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
SQ SEQUENCE 398 AA; 46509 MW; 689BCA5B25CF18BB CRC64;

Query Match 90.3%; Score 1899; DB 11; Length 398;  
Best Local Similarity 89.7%; Pred. No. 2.5e-150;  
Matches 357; Conservative 22; Mismatches 17; Indels 2; Gaps 1;

QY 1 MGANTSRKPVFDEVDNFDHFEILRAIGKSGFGEVCIQVNDTKKCMAMKYNKQKV 60  
DB 1 MGANTSSKAPVFDENEDVNFDFEILRAIGKSGFGKVCIVRKNDTKKCMAMKYNKQKV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPELVNLYSFQDEDMFMVVDLLGGDLRYHLQONVHFKE 120  
DB 61 ERNEVRNVFKELQIMQGLEHPELVNLYSFQDEDMFMVVDLLGGDLRYHLQONVHFQ 120  
QY 121 ETVKLFICELVMDLYLQNRHHRDKPDNILLDEHGHVHTDFNIAAMLPRETOITM 180  
DB 121 DTVKLFICELVMDLYLQNRHHRDKPDNILLDEHGHVHTDFNIAAMLPRETRITV 180  
QY 181 AGTKPYMAPFSSRGAGYSFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240  
DB 181 AGTKPYMAPFSSRGAGYSFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVNMFET 240  
QY 241 TVVTYPSAWSQEWVSLKLLKLEPNPDRFSQSDVQNFYPMNDINWDVAFQKRLIPGIP 300  
DB 241 AIVTYPSAWSQEWVSLKLLKLEPNPDRFSHLTDIQNFYPMNDINWDVAFQKRLIP 300  
QY 301 NKGRLNCDDPTFELEEMILESKEPLHKKKRLAKKEKMDKCDSSQTCLLQHLSDVQKEFI 360  
DB 301 TKGRLNCDDPTFELEEMILESKEPLHKKKRLAKKEKMDKCDSSQTCLLQHLSDVQKEFI 360  
QY 361 IFNREKVNDRPNKQPNLALEQTKD--PQEDGQNNNL 396  
DB 361 IFNREKVSDFNQRQANLALEQTKNTEEBEDGQNNNL 398

RESULT 2  
Q7TPQ4 PRELIMINARY; PRT; 368 AA.

ID Q7TPQ4  
AC Q7TPQ4  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Olfactory epithelium;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Olfactory epithelium;  
RA Strausberg R.,  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC055002; RAH55002.1;  
KW Hypothetical protein.  
SQ SEQUENCE 368 AA; 43213 MW; 0DB7F6977C39BB56 CRC64;

Query Match 82.0%; Score 1726; DB 11; Length 368;  
Best Local Similarity 82.9%; Pred. No. 6.6e-136;  
Matches 330; Conservative 19; Mismatches 17; Indels 32; Gaps 2;

QY 1 MGANTSRKPVFDEVDNFDHFEILRAIGKSGFGEVCIQVNDTKKCMAMKYNKQKV 60  
DB 1 MGANTSSKAPVFDENEDVNFDFEILRAIGKSGFGKVCIVRKNDTKKCMAMKYNKQKV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPELVNLYSFQDEDMFMVVDLLGGDLRYHLQONVHFKE 120  
DB 61 ERNEVRNVFKELQIMQGLEHPELVNLYSFQDEDMFMVVDLLGGDLRYHLQONVHFQ 120  
QY 121 ETVKLFICELVMDLYLQNRHHRDKPDNILLDEHGHVHTDFNIAAMLPRETOITM 180  
DB 121 DTVKLFICELVMDLYLQNRHHRDKPDNILLDEHGHVHTDFNIAAMLPRETRITV 180  
QY 181 AGTKPYMAPFSSRGAGYSFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240  
DB 181 AGTKPYMAPFSSRGAGYSFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVNMFET 240  
QY 241 TVVTYPSAWSQEWVSLKLLKLEPNPDRFSQSDVQNFYPMNDINWDVAFQKRLIPGIP 300  
DB 241 AIVTYPSAWSQEWVSLKLLKLEPNPDRFSHLTDIQNFYPMNDINWDVAFQKRLIP 300  
QY 301 NKGRLNCDDPTFELEEMILESKEPLHKKKRLAKKEKMDKCDSSQTCLLQHLSDVQKEFI 360  
DB 301 TKGRLNCDDPTFELEEMILESKEPLHKKKRLAKKEKMDKCDSSQTCLLQHLSDVQKEFI 360  
QY 361 IFNREKVNDRPNKQPNLALEQTKD--PQEDGQNNNL 396  
DB 331 IFNREKVSDFNQRQANLALEQTKNTEEBEDGQNNNL 368

RESULT 3  
Q7TMD3 PRELIMINARY; PRT; 414 AA.

ID Q7TMD3  
AC Q7TMD3  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 R1 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 R2 [2]  
 R3 SEQUENCE FROM N.A.  
 R4 STRAIN=C57BL/6;  
 R5 STRAUSBERG R.;  
 R6 Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 R7 [3]  
 R8 SEQUENCE FROM N.A.  
 R9 STRAIN=C57BL/6; TISSUE=Brain;  
 R10 STRAUSBERG R.;  
 R11 Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 R12 EMBL; BC052404; AAH52404.1; -;  
 R13 EMBL; BC056396; AAH56396.1; -;  
 R14 Hypothetical protein.  
 R15 SEQUENCE 414 AA; 47916 MW; 3C394415790594F3 CRC64;

Query Match 68.4%; Score 1438.5; DB 11; Length 414;  
 Best Local Similarity 68.5%; Pred. No. 8.1e-112;  
 Matches 280; Conservative 39; Mismatches 71; Indels 19; Gaps 4;  
 QY 1 MGANTSRRPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKQKCV 60  
 DB 1 MCGNHSHPVPVDEENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKQKCV 60  
 QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFE 120  
 DB 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFE 120  
 QY 121 ETVKLFICELVWALDYLNQRIIHRDKPNDILLDEGHVHITDFTNIAAMLPRETQITTM 180  
 DB 121 GTVKLYICELALALEYLQRYHIIHRDKPNDILLDEGHVHITDFTNIAAMLPRETQITTM 180  
 QY 181 AGTKPYMAPEMFS--SRKGAGYSFVADWWSLGVATAYELLGRPPYHRSSTSSKEIVTF 238  
 DB 181 AGTKPYMAPEVQVYVDGPGYSPVDWWSLGVATAYELLGRPPYHRSSTSSKEIVTF 240  
 QY 239 ETTVVYTPSANSQEMVSLKLLKLEPNPDQPSQLSDVQNPYPMNDINWDAVFKELIPGF 298  
 DB 241 KVERVHYSSTWCEGMVSLKLLKLLTKDPSRLSSLDIQSMYTLADWMDAVFKALMPGF 300  
 QY 299 IPNKGRLNCDPTFEEEMILESPLHKKKELAK-KEKDMRKCDSSQTCCLQEHLDVQK 357  
 DB 301 VPKGRLNCDPTFEEEMILESPLHKKKELAKHRSRSDSTKDCSPLNGHLQCCLETYRK 360  
 QY 358 EFIIFNREKVNDRFNKQPNLALRQTKDPOQEDGQNNL 396  
 DB 361 EFIIFNREKLRQGHN-----GQLSDDLGRIGSQTSKQLQDGRNNI 403

RESULT 4  
 Q9JX8 PRELIMINARY; PRT; 414 AA.  
 AC Q9JX8;  
 DT 01-OCT-2000 (TremBLrel. 15, Created)  
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
 DE Serine/threonine protein kinase.  
 GN STK32.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20164328; PubMed=10700184;  
 RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,  
 RA King L., Francomano C., Freisinger P., Spranger S., Marino B.,  
 RA Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,

Goodship J.;  
 "Mutations in a new gene in Ellis-van creveld syndrome and Weyers  
 R1 acrofacial dysostosis.";  
 R2 Nat. Genet. 24:283-286(2000).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AJ250840; CAB76566.1; -;  
 DR HSP; P05132; 1CTP.  
 DR MGD; MGI:1927552; Stk32.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser Thr kinase.  
 DR InterPro; IPR008271; Ser\_thr\_kin\_AS.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 414 AA; 47917 MW; BE394415790B9A13 CRC64;

Query Match 68.3%; Score 1437.5; DB 11; Length 414;  
 Best Local Similarity 69.7%; Pred. No. 9.8e-112;  
 Matches 278; Conservative 38; Mismatches 64; Indels 19; Gaps 3;  
 QY 1 MGANTSRRPPVFDENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKQKCV 60  
 DB 1 MCGNHSHPVPVDEENEDVNFDFHFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKQKCV 60  
 QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFE 120  
 DB 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFE 120  
 QY 121 ETVKLFICELVWALDYLNQRIIHRDKPNDILLDEGHVHITDFTNIAAMLPRETQITTM 180  
 DB 121 GTVKLYICELALALEYLQRYHIIHRDKPNDILLDEGHVHITDFTNIAAMLPRETQITTM 180  
 QY 181 AGTKPYMAPEMFS--SRKGAGYSFVADWWSLGVATAYELLGRPPYHRSSTSSKEIVTF 238  
 DB 181 AGTKPYMAPEVQVYVDGPGYSPVDWWSLGVATAYELLGRPPYHRSSTSSKEIVTF 240  
 QY 239 ETTVVYTPSANSQEMVSLKLLKLEPNPDQPSQLSDVQNPYPMNDINWDAVFKELIPGF 298  
 DB 241 KVERVHYSSTWCEGMVSLKLLKLLTKDPSRLSSLDIQSMYTLADWMDAVFKALMPGF 300  
 QY 299 IPNKGRLNCDPTFEEEMILESPLHKKKELAK-KEKDMRKCDSSQTCCLQEHLDVQK 357  
 DB 301 VPKGRLNCDPTFEEEMILESPLHKKKELAKHRSRSDSTKDCSPLNGHLQCCLETYRK 360  
 QY 358 EFIIFNREKVNDRFNKQPNLALRQTKDPOQEDGQNNL 396  
 DB 361 EFIIFNREKLRQ-----GQHDGQLSDL 383

RESULT 5  
 Q8C4E0 PRELIMINARY; PRT; 414 AA.  
 ID Q8C4E0  
 AC Q8C4E0;  
 DT 01-MAR-2003 (TremBLrel. 23, Created)  
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
 DE Serine/threonine kinase 32.  
 GN STK32.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 DR EMBL; AK082458; BAC38500.1; --  
 DR MGD; MGI:1927552; SCK32.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot.kinase.  
 DR InterPro; IPR002230; Ser\_thr\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot.kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 SQ SEQUENCE 414 AA; 47884 MW; 9C394364BE19E945 CRC64;  
  
 Query Match 68.2%; Score 1434.5; DB 11; Length 414;  
 Best Local Similarity 68.2%; Pred. No. 1.7e-111;  
 Matches 279; Conservative 40; Mismatches 71; Indels 19; Gaps 4;  
  
 QY 1 MGATSRKPPVFDENEDVDFHETLRAIGKSGFGEVCIIVKNDTKKCMKMYNKKCV 60  
 DB 1 MGGNHSKPPVFDENEVDFHETLRAIGKSGFGEVCIIVKNDTKKCMKMYNKKCV 60  
  
 QY 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
 DB 61 ERDEVRNVFRELQIMQGLEHFFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
  
 QY 121 ETVKLFCELMALDYQLQONRIIHRDMKPNILLDEGHVHITDFNIAAMLPRQTITM 180  
 DB 121 GTVKLYICELALALEYQLRYHIIHRDIKPNILLDEGHVHITDFNIAATLVKSGKASSV 180  
  
 QY 181 AGTKPYMAPEMFS--SRKAGYSPAVDWSLGVTAVELLRGRPRYHRSSTSSKEIVHTF 238  
 DB 181 AGTKPYMAPEVQVVDGPGVSPVDWWSLGVTAVELLRGRPRYHRSSTSSKEIVHTF 240  
  
 QY 239 ETTVTVPYSAQSVLSLLKLLPNPQRFSQLSDVQNFPMNDINWDVAFKRLIPGF 298  
 DB 241 KVERVHYSTWCEGVSLKLLTKDPESRLSLRDIQSMTYLADNMWDVAFKALMPGF 300  
  
 QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKLAK-KEKDMKCDSSQTCLLOEHLDSVOK 357  
 DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKLAKRSRDTKDSCLPLNGHLQCCLETVRK 360  
  
 QY 358 EFTIFNREKVRDNFKQPNLALEQTKDPQG-----EDGNNNL 396  
 DB 361 EFTIFNREKLRQQGHN-----GQLSDLGRIQSQTSSKLQDGNNNI 403  
  
 RESULT 6  
 Q9NY57  
 ID Q9NY57 PRELIMINARY; PRT; 414 AA.  
 AC Q9NY57;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE Serine/threonine protein kinase.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;

RX MEDLINE=20164328; PubMed=10700184;  
 RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,  
 RA King L., Francamano C., Freisinger P., Spranger S., Marino B.,  
 RA Dallapicola B., Wright M., Meitinger T., Polymeropoulos M.H.,  
 RA Goodship J.;  
 RT "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers  
 RT acrorenal dysostosis";  
 RL Nat. Genet. 24:283-286 (2000).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AJ250839; CAB76471.1; --  
 DR HSP; P05132; ICTP.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot.kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot.kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 414 AA; 47883 MW; 8PCD58A67EF09B0E CRC64;  
  
 Query Match 67.8%; Score 1425.5; DB 4; Length 414;  
 Best Local Similarity 68.2%; Pred. No. 9.9e-111;  
 Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;  
  
 QY 1 MGATSRKPPVFDENEDVDFHETLRAIGKSGFGEVCIIVKNDTKKCMKMYNKKCV 60  
 DB 1 MGGNHSKPPVFDENEVDFHETLRAIGKSGFGEVCIIVKNDTKKCMKMYNKKCV 60  
  
 QY 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
 DB 61 ERDEVRNVFRELQIMQGLEHFFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
  
 QY 121 ETVKLFCELMALDYQLQONRIIHRDMKPNILLDEGHVHITDFNIAAMLPRQTITM 180  
 DB 121 GTVKLYICELALALEYQLRYHIIHRDIKPNILLDEGHVHITDFNIAATLVKSGRASSM 180  
  
 QY 181 AGTKPYMAPEMFS--SRKAGYSPAVDWSLGVTAVELLRGRPRYHRSSTSSKEIVHTF 238  
 DB 181 AGTKPYMAPEVQVVDGPGVSPVDWWSLGVTAVELLRGRPRYHRSSTSSKEIVHTF 240  
  
 QY 239 ETTVTVPYSAQSVLSLLKLLPNPQRFSQLSDVQNFPMNDINWDVAFKRLIPGF 298  
 DB 241 KVERVHYSTWCKGWALLRKLTKDPESRVSSLDHIQSVPLADNMWDVAFKALMPGF 300  
  
 QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKLAK-KEKDMKCDSSQTCLLOEHLDSVOK 357  
 DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKLAKRSRDTKDSCLPLNGHLQCCLETVRE 360  
  
 QY 358 EFTIFNREKVRDNFKQPNLALEQTKDPQG-----EDGNNNL 396  
 DB 361 EFTIFNREKLRQQGQSLLDTSRGGGQAQSKLQDGCNNL 403  
  
 RESULT 7  
 Q8IY14  
 ID Q8IY14 PRELIMINARY; PRT; 414 AA.  
 AC Q8IY14;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE Serine/threonine protein kinase.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

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RC SEQUENCE FROM N.A.
RA TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038238; AAH38238.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase. Serine/threonine-protein_kinase.
SQ SEQUENCE 414 AA; 47784 MW; F05E8E95FA8242P CRC64;

Query Match 67.6%; Score 1421.5; DB 4; Length 414;
Best Local Similarity 68.2%; Pred. No. 2.1e-110;
Matches 275; Conservative 43; Mismatches 78; Indels 7; Gaps 3;

QY 1 MGNTSRKPPVPDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCAMKYNKQKCV 60
DB 1 MGNHSHKPPVPDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCAMKYNKQKCI 60
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHPKE 120
DB 61 ERDEVRNVFRELEIQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHPTE 120
QY 121 ETVKLFICELVMDLYLQRIIHRDKMPDNILLDEGHVHTIDFNIAAMLPRETQITTM 180
DB 121 GTVKLYICELALALEYLQRIIHRDKMPDNILLDEGHVHTIDFNIAATVKGARSSM 180
QY 181 AGTKPYMAPEFSS--SRGAGYSFVADWMSLGVTAYELLRGRPHIHSSTSSKEIVHTP 238
DB 181 AGTKPYMAPEFQVYMDGGPGYSFVADWMSLGVTAYELLRGRPHIHSVTPIDELNMF 240
QY 239 ETTVTVTYPSAWSQMSVSLKLLLEPNPDRSFLSDVQNFVMDINNDVAFQKRLIPGF 298
DB 241 KVERVHYSTWCKGVALRLKLLTKDPESRSVSLHDIOQVPLADNNDVAFKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKGLAK-KKMDMRKCDSSQTCLLQEHLDVQK 357
DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKGLAKNRSDGTGKSCPLNGHLQHCLETVRE 360
QY 358 EPIIFNREKVRNDFNKRQPNLALQTKDPQG-----EDGQNNL 396
DB 361 EPIIFNREKVRNDFNKRQPNLALQTKDPQG-----EDGQNNL 403

RESULT 8
Q86UX6 PRELIMINARY; PRT; 486 AA.
ID Q86UX6
AC Q86UX6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PKC protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ma A.-H.; Nelson D.A.; Xia L.; Ravi L.; Chen H.-C.; Robinson D.R.;
RA Kung H.-J.;
RT "PKC, A New Human AGC Group Kinase, Phosphorylates SET, a PP2A

Inhibitor.";
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY098866; AAM21719.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 486 AA; 54994 MW; 38FEFBB3863B21F3 CRC64;

Query Match 62.9%; Score 1324; DB 4; Length 486;
Best Local Similarity 64.5%; Pred. No. 3.7e-102;
Matches 254; Conservative 53; Mismatches 77; Indels 10; Gaps 4;

QY 1 MGNTSRKPPVPDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCAMKYNKQKCV 60
DB 72 MSAATARR-PVDFDDKEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCAMKYNKQKCI 130
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHPKE 120
DB 131 ERDEVRNVFRELEIQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHPSE 190
QY 121 ETVKLFICELVMDLYLQRIIHRDKMPDNILLDEGHVHTIDFNIAAMLPRETQITTM 180
DB 191 DTVALYICEMALADYLRGQHIHRDKMPDNILLDEGHVHTIDFNIAATIKDGERATAL 250
QY 181 AGTKPYMAPEFSS--RKGAGYSFVADWMSLGVTAYELLRGRPHIHSSTSSKEIVHTP 238
DB 251 AGTKPYMAPEIFHFSVNGGTGYSFVADWMSVGVNAYELLRGRPHIHSNAVSLVOLF 310
QY 239 ETTVTVTYPSAWSQMSVSLKLLLEPNPDRSFLSDVQNFVMDINNDVAFQKRLIPGF 298
DB 311 STVSQVQVPTWSKEMVALLKLLTVNPEHRLSSLDVQVAPALAGVLDHLSKRVFPGF 370
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKGLAKKKMRKCDSSQT--CLLQEHLDVQK 356
DB 371 VPNGRLNCDPTFELEEMILESPLHKKKKGLAKNRSDGTGKSCPLNGHLQHCLETVRE 430
QY 357 KEPIIFNREKVRNDFNKRQPNLALQTKDPQG 390
DB 431 QDFVFNREKVL-----KRSQDLPREPLPAPERD 459

RESULT 9
Q9JUG4 PRELIMINARY; PRT; 488 AA.
ID Q9JUG4
AC Q9JUG4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Brain cDNA, clone MNCb-1563, similar to AJ250840 serine/threonine
DE protein kinase (Mus musculus).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL;
RA Osada N.; Kusuda J.; Tanuma R.; Ito A.; Hirata M.; Sugano S.;
RA Hashimoto K.;
```

RT "Isolation of full-length cDNA clones from mouse brain cDNA library  
 RT made by oligo-capping method.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AB041542; BAA95027.1; --  
 DR HSSP; P05132; ICTP.  
 DR MGD; MG:2385336; Pke.  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase  
 DR InterPro; IPR002290; Ser Thr kinase.  
 DR InterPro; IPR008271; Ser Thr\_pkin\_AS.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
 KW Hypothetical protein, ATP-binding, Kinase,  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 488 AA; 55276 MW; 310483FF69E24E39 CRC64;  
 Query Match 62.6%; Score 1317.5; DB 11; Length 488;  
 Best Local Similarity 64.3%; Pred. No. 1.3e-101;  
 Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 3;  
 QY 6 SRKPPVFDENEDVNFDFHFIILRAIGKSGFGEVCIVQKNDTKKCMKMYKMKQKCIERDEV 65  
 DB 77 SARRPVFDDKEDVNFDFHFIILRAIGKSGFGEVCIVQKNDTKKCMKMYKMKQKCIERDEV 136  
 QY 66 RNVPFELQIQGLHEHPLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQNVHFKETVKL 125  
 DB 137 RNVPFELQIQGLHEHPLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQNVHFKETVKL 196  
 QY 126 FICELVMDYLDQNRQIHRDKPDNLLDEHGHVHTDFNIAAMLPRETQITTMAGTKP 185  
 DB 197 YICEMALADYLSQHIHRDKPDNLLDEHGHVHTDFNIAATIKDGRATAGTKP 256  
 QY 186 YMAPEMFSS--RKAGYSFADVWMSGLVATYELLGRPRPHIRSSSSKEIVHTFTTVV 243  
 DB 257 YMAPEIFHSGVNGGTGYSFEDVWMSVGMAYELLGRWPRYDIHSSNAVESLQVLFSTVS 316  
 QY 244 TYSANQSEWMSLLKLLPENPDORFQSLSDVQNFPMNDINWDVAFQKRLIPGFIPNKG 303  
 DB 317 QYVPTWSKENVALLRKLLTVNPEHRSFSLQDMQTAFSLAHVLDLSEKKVFGFVFNKG 376  
 QY 304 RLNCDDPTFELEEMILESKPLHKKKKLAKKCKMRKCDSSQT--CLIQEHLDVSQKEFII 361  
 DB 377 RLHCDDPTFELEEMILESRPLHKKKKLAKKNSRDSRDSQSENDYLQDCLDAIQDFVI 436  
 RESULT 10  
 Q8QZV4 ID Q8QZV4 PRELIMINARY; PRT; 488 AA.  
 AC Q8QZV4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical serine/threonine protein kinase.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_taxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RNA SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AB041542; BAA95027.1; --  
 DR EMBL; BC026457; AAB26457.1; --  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser Thr kinase.  
 DR InterPro; IPR008271; Ser Thr\_pkin\_AS.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
 KW Hypothetical protein, ATP-binding, Kinase,  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 488 AA; 55262 MW; 2B6A927BB6B78EF2 CRC64;  
 Query Match 62.6%; Score 1317.5; DB 11; Length 488;  
 Best Local Similarity 64.3%; Pred. No. 1.3e-101;  
 Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 3;  
 QY 6 SRKPPVFDENEDVNFDFHFIILRAIGKSGFGEVCIVQKNDTKKCMKMYKMKQKCIERDEV 65  
 DB 77 SARRPVFDDKEDVNFDFHFIILRAIGKSGFGEVCIVQKNDTKKCMKMYKMKQKCIERDEV 136  
 QY 66 RNVPFELQIQGLHEHPLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQNVHFKETVKL 125  
 DB 137 RNVPFELQIQGLHEHPLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQNVHFKETVKL 196  
 QY 126 FICELVMDYLDQNRQIHRDKPDNLLDEHGHVHTDFNIAAMLPRETQITTMAGTKP 185  
 DB 197 YICEMALADYLSQHIHRDKPDNLLDEHGHVHTDFNIAATIKDGRATAGTKP 256  
 QY 186 YMAPEMFSS--RKAGYSFADVWMSGLVATYELLGRPRPHIRSSSSKEIVHTFTTVV 243  
 DB 257 YMAPEIFHSGVNGGTGYSFEDVWMSVGMAYELLGRWPRYDIHSSNAVESLQVLFSTVS 316  
 QY 244 TYSANQSEWMSLLKLLPENPDORFQSLSDVQNFPMNDINWDVAFQKRLIPGFIPNKG 303  
 DB 317 QYVPTWSKENVALLRKLLTVNPEHRSFSLQDMQTAFSLAHVLDLSEKKVFGFVFNKG 376  
 QY 304 RLNCDDPTFELEEMILESKPLHKKKKLAKKCKMRKCDSSQT--CLIQEHLDVSQKEFII 361  
 DB 377 RLHCDDPTFELEEMILESRPLHKKKKLAKKNSRDSRDSQSENDYLQDCLDAIQDFVI 436  
 RESULT 11  
 Q96BA3 ID Q96BA3 PRELIMINARY; PRT; 369 AA.  
 AC Q96BA3;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

NCBI\_TaxID=9606;  
 (1)  
 RA SEQUENCE FROM N.A.  
 RA TISSUE-Colon;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; BC015792; AAH15792.1; -;  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Hypothetical protein; ATP-binding; Kinase;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 369 AA; 42425 MW; 83C54C4AF7D792E5 CRC64;  
 Query Match 54.1%; Score 1137.5; DB 4; Length 369;  
 Best Local Similarity 62.8%; Pred. No. 9.9e-87;  
 Matches 218; Conservative 47; Mismatches 73; Indels 9; Gaps 3;  
 QY 48 MCAMKYNKQKVERNEVRNFKELQIMQGLEHPELVNLYSFQDEEDMFVVDLLGGD 107  
 DB 1 MYAMKYNKQOCIERDEVRNVRFELEIQIEHVFVNLWYFQDEEDMFVVDLLGGD 60  
 QY 108 LRYHLQNVHFKETVKLFICELVMDLYNQRIIHRDMKPDNILLDEHGHVHTDFNI 167  
 DB 61 LRYHLQNVQFSEDTVRLYICEMALDYLRCQHIIHRDVKPDNILLDEHGHVHTDFNI 120  
 QY 168 AAMLPREQITTMAGTKPYMAPEMPSS--RKAGYSFADVMSLGVTVAYELLGRPPYHI 225  
 DB 121 ATIIKQGERATAGTKPYMAPEIFHSPVNGGTGYSFEVDWMSVGMAYELLGRWPYDI 180  
 QY 226 RSSTSKEIVHTFTVTWYTPSANGQEMVSLIKLLEPNPDRFQSLSDVQNFPMYNDIN 285  
 DB 181 HSSNAVESLVQIFSTVSQVYVFTWSEKEMVALLRKLAVNPEHRLSSLDQVQAAPALAGVL 240  
 QY 286 WDAVFQKRLIPGFI PNKGRLCDPTFELEEMILSKPLKXKRLAKKCKMRKCDSSQT 345  
 DB 241 WDHLSEKRVQFVFNKGRLCDPTFELEEMILSKPLKXKRLAKKCKMRKCDSSQS 300  
 QY 346 --CLLQEHLDVQKEFIIFNREKVRNDFNKRQPNLALQETKDPQGED 390  
 DB 301 ENDYLQDCLDAIQDFVIFNREKL-----KRSQDLPREPLPAPESRD 342  
 RESULT 12  
 Q86UE1 PRELIMINARY; PRT; 369 AA.  
 ID Q86UE1;  
 AC Q86UE1;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE PKE protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Testis;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC045760; AAH45760.1; -;  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 SQ SEQUENCE 369 AA; 42395 MW; E152C66B2D786B4 CRC64;  
 Query Match 54.1%; Score 1137.5; DB 4; Length 369;  
 Best Local Similarity 62.8%; Pred. No. 9.9e-87;  
 Matches 218; Conservative 47; Mismatches 73; Indels 9; Gaps 3;  
 QY 48 MCAMKYNKQKVERNEVRNFKELQIMQGLEHPELVNLYSFQDEEDMFVVDLLGGD 107  
 DB 1 MYAMKYNKQOCIERDEVRNVRFELEIQIEHVFVNLWYFQDEEDMFVVDLLGGD 60  
 QY 108 LRYHLQNVHFKETVKLFICELVMDLYNQRIIHRDMKPDNILLDEHGHVHTDFNI 167  
 DB 61 LRYHLQNVQFSEDTVRLYICEMALDYLRCQHIIHRDVKPDNILLDEHGHVHTDFNI 120  
 QY 168 AAMLPREQITTMAGTKPYMAPEMPSS--RKAGYSFADVMSLGVTVAYELLGRPPYHI 225  
 DB 121 ATIIKQGERATAGTKPYMAPEIFHSPVNGGTGYSFEVDWMSVGMAYELLGRWPYDI 180  
 QY 226 RSSTSKEIVHTFTVTWYTPSANGQEMVSLIKLLEPNPDRFQSLSDVQNFPMYNDIN 285  
 DB 181 HSSNAVESLVQIFSTVSQVYVFTWSEKEMVALLRKLAVNPEHRLSSLDQVQAAPALAGVL 240  
 QY 286 WDAVFQKRLIPGFI PNKGRLCDPTFELEEMILSKPLKXKRLAKKCKMRKCDSSQT 345  
 DB 241 WDHLSEKRVQFVFNKGRLCDPTFELEEMILSKPLKXKRLAKKCKMRKCDSSQS 300  
 QY 346 --CLLQEHLDVQKEFIIFNREKVRNDFNKRQPNLALQETKDPQGED 390  
 DB 301 ENDYLQDCLDAIQDFVIFNREKL-----KRSQDLPREPLPAPESRD 342  
 RESULT 13  
 Q9BGT4 PRELIMINARY; PRT; 368 AA.  
 ID Q9BGT4;  
 AC Q9BGT4;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.



OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecidae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Frontal cortex;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
RT libraries".  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; AB053389; BAB33045.1; -  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Hypothetical protein; ATP-binding; Kinase;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 368 AA; 42218 MW; 5D7269B32DABCC14 CRC64;  
  
Query Match 53.48; Score 1122.5; DB 6; Length 368;  
Best Local Similarity 62.88; Pred. No. 1.8e-85;  
Matches 218; Conservative 44; Mismatches 76; Indels 9; Gaps 3;  
  
QY 48 MCAKYNKQKVERNEVRNVFKELQIMQGLEHPPFLVNLWYSQDEDMFMVVDLLGGD 107  
DB 1 MYAMKYNKQCIERDEVRNVFRELQIEHVFNLWYSQDEDMFMVVDLLGGD 60  
  
QY 108 LRYHLQNVHFKETVKLFCFLWALDYLNQRIHDMKPNILLDEGHVHTDFNI 167  
DB 61 LRYHLQNVQFSDTVRLYICEMALADYLCQRIHDMKPNILLDEGHVHTDFNI 120  
  
QY 168 AAMLPRETQITWAGTKPYNAPEMFSS--RKGAGYFVDMVSLGVTAYELLGRPYHI 225  
DB 121 ATIKQGERATAGTKPYNAPELPHFVNGTGYSFVDMVSLGWAYELLGRPYDI 180  
  
QY 226 RSSTSSKEIVHTFTTIVTTPYSAWSQBMVSLKLLKLEPNPDRPQSLSDVQNPYMDIN 285  
DB 181 HSSNAVESLQVLPSTVSQVPTWSREWVALLKLLTVNFEHRSLSLQDVQAAALAGVL 240  
  
QY 286 WDAVFQRLIPGFIPIKGRNLCDPTFELEMIKSKPLKKGKLAKEKDMKCDSSQT 345  
DB 241 WGHLSKRVPEPDPVFNKGRNLCDPTFELEMIKSKPLKKGKLAKEKDMKCDSSQS 300  
  
QY 346 --CLLQSHLDSVQKEFTIFNREKVRNDRPNKQPNLALEQTKDQGED 390  
DB 301 ENDYLQCLDAIQDFVIFNREKL-----KSLQDLPEPLPAPEPRD 342  
  
RESULT 14  
Q21483 PRELIMINARY; PRT; 379 AA.  
ID Q21483  
AC Q21483  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE M03C11.1 protein.  
GN M03C11.1  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.

RA McMurray A.A.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology."  
RL Science 282:2012-2018(1998).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; Z49128; CA88953.1; -  
DR PIR; T23688; T23688.  
DR HSP; Q63450; IAO6.  
DR WormPep; M03C11.1; CR03492.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc\_1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 379 AA; 43632 MW; 5E2090A1581D27D CRC64;  
  
Query Match 40.11; Score 843.5; DB 5; Length 379;  
Best Local Similarity 44.11; Pred. No. 3.8e-62;  
Matches 158; Conservative 70; Mismatches 117; Indels 13; Gaps 4;  
  
QY 22 HFEILRAIGKSGFGEVCIQKNDTKKCMKMTKQKCVNERNEVRNVFKELQIMQGLEHP 81  
DB 27 HFSVIRSGRAGFGKVCIVQERKTKYKYPALKYMKRERCKEKGVAANVIRELTLSQWSHP 86  
  
QY 82 FLVNLWYSQDEDMFMVVDLLGGDLRYHLQNVHFKETVKLFCFLWALDYLNQRI 141  
DB 87 FIVNLWYTPQDGYMYVMSDLLGGDLRYHLQNVHFKETVKLFCFLWALDYLNQRI 146  
  
QY 142 ITHRMKPNILLDEGHVHTDFNIAMLPRETQITWAGTKPYNAPEMFSS--RKGAG 199  
DB 147 IVHRDIPKPNILLDEGHVHTDFNIAMLPRETQITWAGTKPYNAPEMFSS--RKGAG 206  
  
QY 200 YSFVDMVSLGVTAYELLGRPYHRSSTSSKEIVHTFTTIVTTPYSAWSQBMVSLK 259  
DB 207 YDSRVDMVSLGVTAYELLGRPYHRSSTSSKEIVHTFTTIVTTPYSAWSQBMVSLK 266  
  
QY 260 LLEPNPDRPQSLSDVQNPYMDINWDAVFQRLIPGFIPIKGRNLCDPTFELEMI 319  
DB 267 MLKFDKRLVGLGKLEAKKHSYTERIDFKSVFKKPSFVFPCKGKLNCDPMYELSRILV 326  
  
QY 320 SKPLHKKKRLAKKCKEMKCDSSQTCLEHLDVQKEFTIFNREKVRNDRPNKQPNLA 377  
DB 327 STPIH--RRRTNWNSSGRSSSPQNAALVE----VSKAFIDSRNV-----KIEPN 373  
  
RESULT 15  
Q8WU08 PRELIMINARY; PRT; 166 AA.  
ID Q8WU08  
AC Q8WU08  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to serine threonine kinase 32.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

```

RC TISSUE=Urinary bladder;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; BC021666; AAH21666.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 166 AA; 19792 MW; CDCF94E54C793BA4 CRC64;

Query Match 39.1%; Score 822; DB 4; Length 166;
Best Local Similarity 98.7%; Pred. No. 8e-61;
Matches 155; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGNTSRKPPVPFDENEDVNFDFELRAIGKSGFGEVCIVQKNDTKKCMKMYNKKCV 60
Db 1 MGNTSRKPPVPFDENEDVNFDFELRAIGKSGFGEVCIVQKNDTKKCMKMYNKKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Qy 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEH 157
Db 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEH 157

```

Search completed: June 25, 2004, 10:51:07  
Job time : 46 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 25, 2004, 10:43:09 ; Search time 18 Seconds  
(without alignments)  
1145.543 Million cell updates/sec

Title: US-10-667-442-2

Perfect score: 2104

Sequence: 1 MGANTSRKPPVFDENEDVNF.....NLAEQTKDQGEDGQNNL 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	27.7	444	1 KRAC DICDI	P54644 dictyosteli
2	537	25.1	479	1 PK2 DICDI	P28178 dictyosteli
3	528.5	25.1	648	1 KAPC DICDI	P34099 dictyosteli
4	519	24.7	471	1 KP19 ARATH	Q39030 arabidopsis
5	516.5	24.5	465	1 KP1 ARATH	P42818 arabidopsis
6	513	24.4	680	1 YPK1 YEAST	P12688 saccharomyc
7	511.5	24.3	696	1 SK1 SCHPO	P50530 schizosacch
8	510.5	24.3	352	1 KAPC DROME	P12370 drosophila
9	503	23.9	404	1 KAPC CAEL	P21137 caenorhabdi
10	502.5	23.9	350	1 KAPA CRIGR	P23321 cricetus
11	502.5	23.9	350	1 KAPA FIG	P36887 sus scrofa
12	502.5	23.9	823	1 SCH9 YEAST	P11792 saccharomyc
13	501.5	23.8	740	1 KGA3 HUMAN	P51812 homo sapien
14	501.5	23.8	740	1 KGA3 HUMAN	P18654 mus musculu
15	501	23.8	677	1 YPK2 YEAST	P18961 saccharomyc
16	500.5	23.8	350	1 KAPG HUMAN	P22612 homo sapien
17	500.5	23.8	733	1 KGA2 HUMAN	P15349 homo sapien
18	498.5	23.7	349	1 KAPA CANFA	Q8mj44 canis famil
19	498.5	23.7	350	1 KAPA HUMAN	P17612 homo sapien
20	498.5	23.7	350	1 KAPA RAT	P27791 rattus norv
21	498.5	23.7	350	1 KAPA SHEEP	Q9mzd9 ovis aries
22	498.5	23.7	689	1 ARK1 HUMAN	P25098 homo sapien
23	496.5	23.6	350	1 KAPA BOVIN	P00517 bos taurus
24	496.5	23.6	733	1 KGA2 MOUSE	Q9wt33 m ribosomal
25	496	23.6	350	1 KAPB MOUSE	P05206 mus musculu
26	495.5	23.6	586	1 KPCI MOUSE	Q62074 mus musculu
27	495.5	23.6	587	1 KPCI HUMAN	P41743 homo sapien
28	494.5	23.5	752	1 KGA2 CHICK	P18652 gallus gall
29	493.5	23.5	398	1 KAPC YEAST	P05986 saccharomyc
30	493.5	23.5	646	1 KDBE SCHPO	Q10364 schizosacch
31	493.5	23.5	689	1 ARK1 BOVIN	P21146 bos taurus
32	493	23.4	689	1 ARK1 MESAU	Q64682 mesocricetu
33	492.5	23.4	350	1 KAPA_MOUSE	P05132 mus musculu

ALIGNMENTS

RESULT 1

ID	KRAC DICDI	STANDARD;	PRT;	444 AA.
AC	P54644;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	RAC-family serine/threonine kinase homolog (EC 2.7.1.-).			
GN	PKBA OR DAGA.			
OS	Dictyostelium discoideum (Slime mold).			
OC	Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.			
OX	NCBI_TaxID=44689;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AX3;			
RA	Moore B., Haribabu B., Rabino M., Ortiz B., Reichel G., Skehel P., Williams J., Bouzid S., Veron M., Dotti R.P.;			
RL	Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. RAC			
CC	SUBFAMILY. STRONGEST TO YEAST YPK1/YPK2.			
CC	-1- SIMILARITY: Contains 1 PH domain.			

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DR	HSSP; U15210; AAA76692.1; --			
DR	DictyBase; DB0003794; pkba.			
DR	InterPro; IPR001849; PH.			
DR	InterPro; IPR000961; Pkinase_C.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR008271; Ser_thr_pkin_AS.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			
DR	Pfam; PF00169; PH; 1.			
DR	Pfam; PF00069; Pkinase; 1.			
DR	Pfam; PF00433; Pkinase_C; 1.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00233; PH; 1.			
DR	SMART; SM00133; S_TK_X; 1.			
DR	SMART; SM00220; S_TK; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00003; PH_DOMAIN; 1.			
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.			
FT	DOMAIN 5 100 PH.			
FT	DOMAIN 120 374 PROTEIN KINASE.			
FT	NP BIND 126 134 ATP (BY SIMILARITY).			
FT	BINDING 149 149 ATP (BY SIMILARITY).			
FT	ACT SITE 243 243 BY SIMILARITY.			
SQ	SEQUENCE 444 AA; 51062 MW; 12367A1A11C5680 CRC64;			

Query Match 27.7%; Score 582.5; DB 1; Length 444;  
 Best Local Similarity 38.2%; Pred. No. 8.6e-33;  
 Matches 120; Conservative 70; Mismatches 109; Indels 15; Gaps 6;

QY 4 NTSRKPVPDENEDVDFHFEILRAIGKSGFGEVCIQKNDTKQKCMKMKQKQKCVERN 63  
 DB 104 NGGKQP---KKSEKVGADPELLNLVKGSGFGKVIQVKOTGEVYAMKVLKSHVHN 160

QY 64 EVNRVFKELQIMQGLEHPLVNLWYSFQDEEDPMVVDLLGDLRLYLQONVHFKEETV 123  
 DB 161 EVEHTLSERNILQINHPFLVNLNYSFQDEKLYFILDYVNGGELFYHLQKCKFTEDRV 220

QY 124 KLFCELVAMALDYQONRIIHRDKMPDNILLDEGHVHTDNLIA--AMLPRETOITMA 181  
 DB 221 RYGAELVLALEHLHLSGVYRDLPENLLLTNEGHCMTDGLCKEGLLTPDKTGTCF 280

QY 182 GTPYMAPEPSSRKGAGYSFVNDWWSLGVYAYELLRGRPRYHRSSTSSKEIVHTPETT 241  
 DB 281 GTPYLAPEVL---QNGYKQVDWWSFGSLLYEMLTGLPPFY---NQDQVYRKMME 334

QY 242 VVTYPSAWSEMSVLLKLLPNDPQPSQLSDVQNPFPYNDINWDAVQKRLIPGIPN 301  
 DB 335 KLSFPHPISPDARSLLRQLLDEPKELADPNLIKRPFRFSIDWEOQFQKNIPPPPIPN 394

QY 302 -KGRLN---CDPTF 311  
 DB 395 VKGSADTSQIDPVF 408

## RESULT 2

ID PK2 DICDI STANDARD; PRT; 479 AA.

AC P8178; DB 104 NGGKQP---KKSEKVGADPELLNLVKGSGFGKVIQVKOTGEVYAMKVLKSHVHN 160

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Protein kinase 2 (EC 2.7.1.-).

GN PKGB OR PKA.

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

OX NCBI\_TaxID=44689;

RN [1]

RX MEDLINE=91142122; PubMed=1996312;

RA Haribabu B., Dotti R.P.;

RT "Identification of a protein kinase multigene family of Dictyostelium discoideum: molecular cloning and expression of a cDNA encoding a developmentally regulated protein kinase."

RL Proc. Natl. Acad. Sci. U.S.A. 88:1115-1119(1991).

CC -1- DEVELOPMENTAL STAGE: KINASE 2 ENCODES A 2.0 KB AND A 2.2 KB TRANSCRIPT. THE SMALLER ONE IS EXPRESSED IN VEGETATIVE CELLS, AND THE LARGER ONE DURING DEVELOPMENT.

CC -1- INDUCTION: The 2.2 kb transcript is probably induced by exogenous CAMP via a cell-surface receptor-mediated signal transduction pathway.

CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6 kinase subfamily.

CC -----

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CC -----

CC EMBL; M59744; AAA33186.1; .

CC PIR; A38578; A38578.

CC HSSP; P05132; 1CTP.

CC DictyBase; DDB0002054; pkgb.

CC InterPro; IPR000961; Pkinase\_C.

CC InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.

DR InterPro; IPR002290; Ser\_thr\_pkinase.

DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00433; pkinase C; 1.

DR PRINTS; PRO0109; TYRKINASE.

DR PRODOM; PD000001; Prot\_kinase; 1.

DR SMART; SM00133; S\_TK\_X; 1.

DR SMART; SM00220; S\_TKC; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding; CAMP;

KW Phosphorylation.

FT DOMAIN 53 60 POLY-GLN.

FT DOMAIN 73 77 POLY-GLN.

FT NP BIND 153 407 PROTEIN KINASE.

FT BINDING 159 167 ATP (BY SIMILARITY).

FT BINDING 182 182 ATP (BY SIMILARITY).

FT ACT SITE 276 276 BY SIMILARITY.

FT MOD\_RES 309 309 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

SQ SEQUENCE 479 AA; 52963 MW; E0015C08E3J7105 CRC64;

Query Match 25.5%; Score 537; DB 1; Length 479;  
 Best Local Similarity 36.2%; Pred. No. 1.2e-29;  
 Matches 117; Conservative 66; Mismatches 124; Indels 16; Gaps 6;

QY 11 VPDEN-EDVNFHFEILRAIGKSGFGEVCIQKNDTKQKCMKMKQKQKCVERNVNF 69  
 DB 140 IFSKNQKSATKODPELLNLVKGSGFGKVIQVKOTGEVYAMKVLKSHVHN 199

QY 70 KELQIMQGLEHPLVNLWYSFQDEEDPMVVDLLGDLRLYLQONVHFKEETV 129  
 DB 200 SEKTIQCTSHHPFVNLHYAFQTKLYWVDFVNGGELFYHLKREGFSEPRVKIYAE 259

QY 130 LVNADYLQONRIIHRDKMPDNILLDEGHVHTDNLIAAMLPRETOITMAGTKPYMAP 189  
 DB 260 IVSALDHLKQDIVYRDLPENILLDEGHVHTDNLIAAMLPRETOITMAGTKPYMAP 319

QY 190 EMFSSRKGAGYSFVNDWWSLGVYAYELLRGRPRYHRSSTSSKEIVHTPETT 249  
 DB 320 EVLN---GHGHCADVNDWWSLGLTYLLYEMLTGLPPFYQNVSTMYQKINGSLKLPY---I 373

QY 250 SQEMVSLKLLPNDPQPSQL---SDVQNPFPYNDINWDAVQKRLIPGIP 303  
 DB 374 SPEAKSLLLEGLLTREVDYKLTGKGGGKQHPFKKIDWEKLDKEVEVHFKPKVKSGTD 433

QY 304 RLNCDDPTFELE---EMILSKPL 323  
 DB 434 ISQIDPVFTQERPMDSLVETSAL 456

## RESULT 3

ID KAPC DICDI STANDARD; PRT; 648 AA.

AC P34039;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DR CAMP-dependent protein kinase catalytic subunit (EC 2.7.1.37).

GN PKAC OR PK2 OR PK3.

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

OX NCBI\_TaxID=44689;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91333730; PubMed=1864510;

RA Buerki E., Anjard C., Scholder J.-C., Reymond C.D.;

RT "Isolation of two genes encoding putative protein kinases regulated during Dictyostelium discoideum development."

RL Gene 102:57-65(1991).

RN [2]

RP CHARACTERIZATION.

127 QY ICELVMALDYLQNR.IIHRDMKPDNLLDGHGVHITDFNIAAMLPREQTITTMAGTKPY 186  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 440 DB AAEIVLALEFLHKQNIVTRDLKXPNELLIDNQGHIKITDFGFAKV--EDRTFTLCGTPEY 497  
 167 QY WAPENFSSRGKAGYSFANDVNSLSGYTVAYELLGRSPYHIRSTSSKEIVHTPTTWTVP 246  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 498 DB LAPETIIQSQ---GHGKADVMAUGLIIFEMLAGYPFFY---DDDTFAIYNKILAGRITFP 551  
 247 QY SAWSOEWMSLLKKLLPENPQQRFSQLS-----DVQNPPYMNDINDAVFQKRITFGPIPK 302  
 :|:|:|:|:~::~||:|:~::||:|:~::||:|:~::||:|:~::||:|:~::||:|:~::||:|:~::||:|:~::||:|:  
 552 DB LGFDVDAXDLIKRLTADRTRELGA LKOGALDVKNHRFSDINWERLYQRDRNGPIPKI 611  
 303 QY GR LNC DPT F E L -- R E M I L E S K P 322  
 :|:|:|:|:~::~||:|:~::||:|:~::||:|:~::||:|:~::||:|:~::||:|:~::||:|:~::||:|:~::||:|:  
 612 DB QRQGDSNNPFMYDESEWVEEPP 633

### RESULT 4

ID	XP19 ARATH	STANDARD;	PRT; 471 AA.
AC	Q39030; Q949XS; Q9CSR1;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	15-WAR-2004 (Rel. 43, Last annotation update)		
DE	Serine/threonine-protein kinase AtPK19 (SC 2.7.1.-) (Ribosomal-protein S6 kinase homolog).		
GN	ATPK19 OR AT3G08720 OR F17014.19.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosoids II; Brassicales; Brassicaceae; Arabidopses.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Columbia;		
RX	MEDLINE=95129712; PubMed=7828736;		
RA	Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kanada H., Shinozaki K.;		
RT	"Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold or salinity stress in Arabidopsis thaliana.";		
RL	FEMS Lett. 398:199-204(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Columbia;		
RX	MEDLINE=21016720; PubMed=1130713;		
RA	Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M., Farmanm B., Boutry M., Bloeker H., Perez-Alonso M., Obermaier B., Delenay M., Gally G., Griwell L.A., Maché R., Puigdomenech P., De Simone V., Choïsne N., Artiguenave F., Robert C., Brottier P., Wincker P., Cattolico L., Weissgenau J., Saunin W., Quettier F., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V., Wurdeleann R., Drzonek H., Erfle H., Jordan N., Bangart S., Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G., Vezi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B., Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G., Reichelt J., Scharfe M., Schoen O., Argues M., Terol J., Climent J., Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D., Cooke R., Laude M., Berger-Lilauro C., Purnelle B., Masuy D., de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casasuberta E., Montfort A., Agiriau A., Flores M., Liguori R., Vitale D., Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J., Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P., Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.S., Feldbiyhu T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.I., White O., Venter J.C., Fraser C.M., Kaneke T., Nakamura Y., Sato S., Kato T., Asamizu E., Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;		
RT	"Sequence and analysis of chromosome 3 of the plant Arabidopsis"		

thaliana."; [3]  
 RN Nature 408:820-822(2000).  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=cv. Columbia;  
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,  
 Palm C.J., Theologis A., Ecker J., Davis R.W.;  
 RL Submitted (Nov-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RP MEDLINE=22954850; PubMed=145931172;  
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
 Karlin-Neumann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
 Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
 Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
 Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
 Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.P.,  
 Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Karnes M.,  
 Khan S., Koesema B., Ishida J., Jiang P.X., Jones T., Kawai J.,  
 Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
 Satou M., Tanse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,  
 Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RT "Empirical analysis of transcriptional activity in the Arabidopsis  
 genome."; Science 302:842-846(2003).  
 RL Science 302:842-846(2003).  
 CC -!- FUNCTION: May be involved in adaptation of plant to cold or high-  
 salt conditions.  
 CC -!- PTM: Undergoes serine-specific autophosphorylation (By  
 similarity).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6  
 Kinase subfamily.  
 CC -!- CAUTION: Ref.4 sequence differs from that shown due to a  
 frameshift in position 391.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; D42061; BAA07661.1; -;  
 DR EMBL; AC012562; AAG51345.1; -;  
 DR EMBL; AF325094; AAK17162.1; -;  
 DR EMBL; AY050826; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; S68463; S68463.  
 DR HSSP; P05132; 1CTP.  
 DR InterPro; IPR000961; Pkinase.C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00433; pkinase.C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transphosphatase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 140 395 PROTEIN\_KINASE.  
 FT NP\_BIND 146 154 ATP (BY SIMILARITY).  
 FT BINDING 169 169 ATP (BY SIMILARITY).  
 FT ACT\_SITE 263 263 BY SIMILARITY.  
 FT CONFLICT 250 250 A -> V (IN REF. 1).  
 FT CONFLICT 359 360 LS -> VF (IN REF. 1).  
 SQ SEQUENCE 471 AA; 53037 MW; 95F007B44B58DFB5 CRC64;  
 Query Match 24.7%; Score 519; DB 1; Length 471;

Best Local Similarity 34.0%; Pred. No. 28-28;  
 Matches 108; Conservative 64; Mismatches 122; Indels 24; Gaps 4;  
 QY 12 PDENED-----VNFDPHEILRAIGKSGFGEYVICVQKNDTKKQKAMKYNKOK 58  
 DB 116 FSGNDTDSKSPSEVSGVVGIEDFEVLKVVQGGAFKGYQVKKDTSEIYAMKVKRDK 175  
 QY 59 CYVERNEVRNVFKELQIMQGLEHPLVNLWYSQDEDMFVVDLLGGDLRYHLQONVHP 118  
 DB 176 IVEKNHAYTKAERDILTIDHPFVQLKYSFQTKYRLYLVLDFINGGHLFPQLYHQGLF 235  
 QY 119 KEETVKLFICELVMDLYLQNOIRIHRDMKPNILIDHGHVHITDENTIAAMLPRETOIT 178  
 DB 236 REDLARKVTTAEIVSAVSHLHEGIMHRDLPENILMDVGHVNLDTDFGLAKPEETRSN 295  
 QY 179 TWAGTKPYMAPEMFSRKGAGYSFVDMWSLGVYATYELLGRPRPYHIRSTSKEIVHTF 238  
 DB 296 SMCGTTEYMAPEIV--RGKGDHKAADMSVGLLYEMLTGKPPPLGSGKIQKIV-- 349  
 QY 239 EITVTVTPSAWQSEVSLIKLLEPNPDQRF-----SOLSDVQVFPFYMNDINNDVAFQKEL 294  
 DB 350 -KDKIKLPOFLSNEAHLKGLLQKPEPRLGSGPGBEIKKHKWKAINWKJLAREV 408  
 QY 295 IPGFIPNKGRLNCDPTFE 312  
 DB 409 QPSFKPAVSGRQCIAFD 426  
 RESULT 5  
 ID\_KPK1 ARATH STANDARD; PRT; 465 AA.  
 AC P42818;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Serine/threonine-protein kinase AtPK1/AtPK6 (EC 2.7.1.1).  
 GN ATPK1 OR ATPK6 OR AT3G08730 OR F17014.20.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopses.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Landsberg erecta;  
 RX MEDLINE=94292519; PubMed=7912697;  
 RA Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;  
 RT "AtPK1, a novel ribosomal protein kinase gene from Arabidopsis. I.  
 RT Isolation, characterization, and expression."; J. Biol. Chem. 269:17586-17592(1994).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RP MEDLINE=95129712; PubMed=7828736;  
 RX Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kanada H.,  
 RA Shinozaki K.;  
 RT "Two genes that encode ribosomal-protein S6 kinase homologs are  
 RT induced by cold or salinity stress in Arabidopsis thaliana."; FEBS Lett. 358:199-204(1995).  
 RL [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RP MEDLINE=21016720; PubMed=11130713;  
 RX Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,  
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,  
 RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
 RA De Simone V., Choien N., Artiguenave F., Robert C., Brottier P.,  
 RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
 RA Wurmbach E., Drzonenek H., Erflie H., Jordan N., Bangert S.,  
 RA Wedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,  
 RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,  
 RA Navarro P., Collado C., Perez-Perez A., Ottenswaelder B., Duchemin D.,  
 RA Cooke R., Laudie M., Berger-Liauro C., Fumelle B., Masuy D.,  
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
 RA Monfort A., Agirion A., Flores M., Liguori R., Vitale D.,  
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,  
 RA Crasay T.H., Haase B., Wai R., Wu D., Peterson J., Van Aken S.,  
 RA Pal G., Millescher J., Sellers P., Gill J.W., Feldblyum T.V.,  
 RA Preuss D., Lin X., Niemman W.C., Salzberg S.L., White O., Venter J.C.,  
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakayama S., Nakazaki N., Shimpō S., Takeuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
 RT thaliana";  
 RL Nature 408:820-822(2000).  
 RN [4]  
 RP CHARACTERIZATION  
 RC STRAIN=cv. Landsberg erecta;  
 RX MEDLINE=94292520; PubMed=8021267;  
 RA Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb C.J.;  
 RT "Atpki, a novel ribosomal protein kinase gene from Arabidopsis. II.  
 RT Functional and biochemical analysis of the encoded protein.";  
 RL J. Biol. Chem. 269:17593-17599(1994).  
 CC -1- FUNCTION: Could be involved in the control of plant growth and  
 CC development. Phosphorylates two ribosomal proteins, P14 and P16.  
 CC -2- TISSUE SPECIFICITY: Expressed in all tissues.  
 CC -3- DEVELOPMENTAL STAGES: Predominates during high metabolic activity  
 CC in growing buds, root tips, leaf margins and germinating seeds.  
 CC -4- PMW: Undergoes serine-specific autophosphorylation.  
 CC -5- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6  
 CC kinase subfamily.  
 CC -----  
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 CC -----  
 CC EMBL; L29030; AAA21142.1; -;  
 CC EMBL; D42056; BAA07656.1; -;  
 CC EMBL; AC012562; AAG51351.1; -;  
 CC PIR; S68462; S68462.  
 CC HSSP; Q63450; 1A06.  
 CC InterPro; IPR000961; Pkinase C.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR008271; Ser\_thr\_kin\_AS.  
 CC InterPro; IPR002290; Ser\_thr\_kinase.  
 CC Pfam; PF00069; pkinase; 1.  
 CC Pfam; PF00433; pkinase\_C; 1.  
 CC ProDom; PD000001; Prot\_kinase; 1.  
 CC SMART; SM00133; S TK X; 1.  
 CC SMART; SM00220; S TK; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 KW DOMAIN 134 389 PROTEIN KINASE  
 FT NP\_BIND 140 148 ATP (BY SIMILARITY).  
 FT BINDING 163 163 ATP (BY SIMILARITY).  
 FT ACT\_SITE 257 257 BY SIMILARITY.  
 FT MUTAGEN 163 163 K->R: ACTIVITY SUBSTANTIALLY DIMINISHED.  
 SQ SEQUENCE 465 AA; 52588 MW; 407133D674CA271F CRC64;  
 Query Match 24.5%; Score 516.5; DB 1; Length 465;  
 Best Local Similarity 34.1%; Pred. No. 2.9e-28;  
 Matches 102; Conservative 66; Mismatches 120; Indels 11; Gaps 3;

QY 18 VNFDPHFEILRAIGKSGFGEYCIQKNDTKKQCAKMYKQKCVNEVNVFKEQLQMOG 77  
 DB 129 VGIDDFEWMKVGKGAFKGYQVRKETSSEIYAMKVRKDHMEKNAEYMAERDILTK 188  
 QY 78 LEHPFLVNLWYSQDEBEMVVDLLIGGLDRLYHLQONVHFKEBTVKLFICELVMDYL 137  
 DB 189 IDHPFIVQLKYSQTKYKRLVLDLPFNGHLFQLYHQGLFREDLARVYTAIEIVSAVSHL 248  
 QY 138 ONQRIHRDKMPNILLDEHGHVHTDNTAAMLPRTOITTMAGTQYVWAPENFSSRKG 197  
 DB 249 HEKGIMRDLKPNILMDTGHVNLTDGFLAKGFEENTRSNMGCTTETYNAPETIV--RG 305  
 QY 198 AGVSFADVMSLGVTAVELLGRPRVHRSSTSKBIVHTFETVTVVPSAWSOBMSVSL 257  
 DB 306 KGHDKAADWWSVGLLYEMLTGKPPFLGSGKTKQKIV----KDKIKLPQFLSNEARAIL 361  
 QY 258 KLLLEPNPQDQ----FSQLSDVQNFYPMNDINDAVFQKRLIPGIPNKRLNCDPTFE 312  
 DB 362 KGLLQKEPERRLGLSGLGAEEIKQHKWFKGINNKKLEAREVMPSPKFEVSGRQCIANFD 420  
 RESULT 6  
 YPK1 YEAST  
 ID YPK1 YEAST STANDARD; PRT; 680 AA.  
 AC P12688;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Serine/threonine-protein kinase YPK1 (EC 2.7.1.-).  
 GN YPK1 OR YKL126W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89090805; PubMed=2850145;  
 RA Maurer R.A.;  
 RT "Isolation of a yeast protein kinase gene by screening with a  
 RT mammalian protein kinase cDNA";  
 RL DNA 7:469-474(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rad M.R., Xu G., Kirchath L., Fritz C., Keuchel H., Hollenberg C.P.;  
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP DISCUSSION OF SEQUENCE.  
 RX MEDLINE=93173125; PubMed=8437590;  
 RA Chen P.C., Lee K.S., Levin D.E.;  
 RT "A pair of putative protein kinase genes (YPK1 and YPK2) is required  
 RT for cell growth in Saccharomyces cerevisiae";  
 RL Mol. Gen. Genet. 236:443-447(1993).  
 CC -1- FUNCTION: Plays an essential role in the proliferation of yeast  
 CC cells.  
 CC -2- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC RAC SUBFAMILY. STRONGEST TO YPK2.  
 CC -----  
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 CC -----  
 CC EMBL; M21307; AAA34880.1; -;  
 CC EMBL; Z28126; CAA81967.1; -;  
 CC PIR; S37955; S37955.  
 CC HSSP; P05132; 1CTP.  
 CC Germonline; 139882; -;  
 CC SGB; S0001609; YPK1.  
 CC GO; GO:0005935; C:bud neck; IDA.







```

DR InterPro; IPR008271; Ser thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot.Kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; CAMP;
KW Phosphorylation; Myristate; Lipoprotein.
FT INVT_MET 0 0 BY SIMILARITY.
FT LIPID 1 1 N-myristoyl glycine (By similarity).
FT DOMAIN 45 299 PROTEIN_KINASE.
FT NP_BIND 51 59 ATP (BY SIMILARITY).
FT BINDING 74 74 ATP (BY SIMILARITY).
FT ACT_SITE 168 168 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40707 MW; 8842BCFA95E9640 CRC64;

Query Match 24.3%; Score 510.5; DB 1; Length 352;
Best Local Similarity 34.4%; Pred. No. 5.5e-28;
Matches 110; Conservative 72; Mismatches 119; Indels 19; Gaps 6;

QY 21 DFEFLRAIGKSGFCEVICQNDTKMKCMKMYMKQKVERNEVRNVFKELQIMQGLEH 80
DB 43 DDFEIKTLGTSGFGRVIMVHKPTKDYVMKILDKQVKVLKQVEHTLNEKRILQAIOF 102
QY 81 PFLVNLMTYSFQDEDMFMVVDLLGLGDLRYHLQNVHFKETVKLFICELVVALDYLNQ 140
DB 103 PFLVSLRVHFQNSLNLYLVPGEMPSHLRKVRSEPHSRFYAAQIVLAPYLHYL 162
QY 141 RIIHDMKPDNILLDEGHVHTIDNIAMLPRETQITMTACTKPYMAPEMPSSKKGAGY 200
DB 163 DLIVRDLKPNLLDSQGYLKVTDGFAKRVKGR--WTLCTGPEYLAPEILSK--GY 217
QY 201 SFADVWSISGVTAYELLGRRRYPYHRSSTSSKEIVHTPTTV---VTYPSAQSQEWISL 257
DB 218 NKADVWALGVLYVMAAGYPPFF-----ADQPIQVEKIVSGKVRFPSPHSGSLKDLL 271
QY 258 KKLLEPNPQRFSQL-----SDVQNPFFYMDINWDAVFKRLIFGIPN-KGLNCDPTFE 312
DB 272 RNLQVQLTKRYGNLKAGVNDIKNQWPASTDWIAIFQKIEAPFIPCKGPGDTSNFD 331
QY 313 LEEMILESPLHKKKRLAK 332
DB 332 YEAEALRISSTKCAKEFAE 351

RESULT 9
KAPC_CABEL STANDARD; PRT; 404 AA.
AC KAPC_CABEL 018310; O18311;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP-dependent protein kinase catalytic subunit (EC 2.7.1.37) (PKA C).
GN Kin-1 OR ZK909.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI TaxID=6239;
RN [1]_SEQUENCE FROM N.A. (ISOFORM B).
RP STRAIN=Bristol N2;
RX MEDLINE=90216721; PubMed=2324104;
RA Gross R.E., Bagchi S., Lu X., Rubin C.S.;
RT "Cloning, characterization, and expression of the gene for the
RT catalytic subunit of cAMP-dependent protein kinase in Caenorhabditis
RT elegans. Identification of highly conserved and unique isoforms
RT generated by alternative splicing."

```

```

RL J. Biol. Chem. 265:6896-6907 (1990).
RP [2]
RC STRAIN=Bristol N2;
RA White S., McLay K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Durbán R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Composed of two regulatory chains and two catalytic
CC chains.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=13;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=e;
CC IsoId=P21137-1; Sequence=Displayed;
CC Name=a; Synonym=Major;
CC IsoId=P21137-2; Sequence=VSP_004751, VSP_004758;
CC Name=b; Synonym=Minor;
CC IsoId=P21137-3; Sequence=VSP_004751;
CC Name=c;
CC IsoId=P21137-4; Sequence=VSP_004756, VSP_004757;
CC Name=d;
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CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. cAMP
CC subfamily.
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GN PRKACA.  
 OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus.  
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 RA Howard P., Day K.H., Kim K.E., Richardson J., Thomas J., Abraham I.,  
 RA Fleischman R.D., Gottesman M.M., Maurer R.A.;  
 RT "Decreased catalytic subunit mRNA levels and altered catalytic  
 RT subunit mRNA structure in a cAMP-resistant Chinese hamster ovary cell  
 RT line.";  
 RL J. Biol. Chem. 266:10189-10195(1991).  
 CC -1- FUNCTION: Phosphorylates a large number of substrates in the  
 CC cytoplasm and the nucleus.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- ENZYME REGULATION: Activated by cAMP.  
 CC -1- SUBUNIT: A number of inactive tetrameric holoenzymes are produced  
 CC by the combination of homo- or heterodimers of the different  
 CC regulatory subunits associated with two catalytic subunits. cAMP  
 CC causes the dissociation of the inactive holoenzyme into a dimer of  
 CC regulatory subunits bound to four cAMP and two free monomeric  
 CC catalytic subunits.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and  
 CC monomeric catalytic subunit). Translocates into the nucleus  
 CC (monomeric catalytic subunit) (By similarity).  
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed in mammalian tissues.  
 CC -1- PIM: Asn-2 is partially deaminated to Asp-2 giving rise to 2  
 CC major isoelectric variants, called CB and CA respectively (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC -1- CAMP subfamily.  
 CC  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC  
 DR EMBL; M63311; AAA37010.1; -  
 DR PIR; B40384; OKHYCA.  
 DR HSRP; P05132; ICRP.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_kin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00433; pkinase C; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00133; S TK X; 1.  
 DR SMART; SM00220; S TKX; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 DR Transferrase; Serine/threonine-protein kinase; Nuclear protein; cAMP;  
 KW ATP-binding; Myristate; Phosphorylation; Multigene family;  
 KW Lipoprotein.  
 FT INIT\_MET 0 0 BY SIMILARITY.  
 FT DOMAIN 43 297 PROTEIN KINASE.  
 FT NP\_BIND 49 57 ATP (BY SIMILARITY).  
 FT BINDING 72 72 ATP (BY SIMILARITY).  
 FT ACT\_SITE 166 166 N-myristoyl glycine (By similarity).  
 FT LIPID 1 1 BY SIMILARITY.  
 FT MOD\_RES 2 2 DEAMINATION (PARTIAL) (BY SIMILARITY).  
 FT MOD\_RES 10 10 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 139 139 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 197 197 PHOSPHORYLATION (BY SIMILARITY).

FT MOD\_RES 338 338 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 350 AA; 40488 MW; 2FC89F73A0DB53D CRC64;  
 Query Match 23.9%; Score 502.5; DB 1; Length 350;  
 Best Local Similarity 34.0%; Pred. No. 1.9e-27;  
 Matches 99; Conservative 76; Mismatches 97; Indels 19; Gaps 6;  
 QY 21 DHPFELRAIGKSGFGEVCIQKNDTKKCMKMYMKOKCVERNEVNVFKELQIMQGLEH 80  
 DB 41 DHPDRIKTGTGSGFGRVLMVKGKGTGNHYAMKILDKQVVKLQKIEHTLNKRGILQAVNF 100  
 QY 81 PFLVNIWYFOBEDMFVVDLLGLGDLRYHLQNVHFKEBTVKLFICELVMDALDYLNQ 140  
 DB 101 PFLVVKLEFQKNSNLYWMEVPGGEMFSLHRIGRFSEPHARFPAQIVLTFFYLHSL 160  
 QY 141 RIHRDMKPDNILLDEHGHVHTDFNIAAWLPRETQITTWAGTKPYNAPMPSRRKAGY 200  
 DB 161 DLTYRDLKPENLIDQGYIQVTFGFAKRVKGR--WTLGCTPYELAPILSK---GY 215  
 QY 201 SPAYDMSVSGVTAYELLGRRPVHRSSTSSKSIHVHTFTV---VTPSAMSQEMVSL 257  
 DB 216 NKAVDHWALGVLYEWAAGYPPPF-----ADQPIQIYKIVSGKRVFPHFSSDLKDLL 269  
 QY 258 KKLLEPNPQRFSQL----SDVQNFYPMNDINWDVAFQKRLIPGPIFN-KG 303  
 DB 270 RNLLQVDLTKRFGNLGNGVNDIKNKHKEATTDWIAIYQKRVAPFIPKFG 320  
 RESULT 11  
 KAPA\_PIG  
 ID\_KAPA\_PIG STANDARD; PRT; 350 AA.  
 AC P36857;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE CAMP-dependent protein kinase, alpha-catalytic subunit (EC 2.7.1.37)  
 DE (PKA C-alpha).  
 GN PRKACA.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE OF 194-350 FROM N.A.  
 RX MEDLINE=87304251; PubMed=2441988;  
 RA Adavani S.R., Schwarz M., Showers M.O., Maurer R.A., Hemmings B.A.;  
 RT "Multiple mRNA species code for the catalytic subunit of the cAMP-  
 RT dependent protein kinase from LLC-PK1 cells. Evidence for two forms  
 RT of the catalytic subunit.";  
 RL Eur. J. Biochem. 167:221-226(1987).  
 RN [2]  
 RP SEQUENCE OF 1-7, MYRISTOYLATION, AND DEAMINATION OF ASN-2.  
 RX MEDLINE=98180418; PubMed=9521123;  
 RA Jedrzejewski P.T., Girod A., Tholey A., Koenig N., Thullner S.,  
 RA Kinzel V., Bossemeyer D.;  
 RT "A conserved deamidation site at Asn 2 in the catalytic subunit of  
 RT mammalian cAMP-dependent protein kinase detected by capillary LC-MS  
 RT and tandem mass spectrometry.";  
 RL Protein Sci. 7:457-469(1998).  
 RN [3]  
 RP DEAMINATION OF ASN-2, AND SUBCELLULAR LOCATION.  
 RX MEDLINE=20153511; PubMed=10684253;  
 RA Pepperkok R., Hotz-Wagenblatt A., Koenig N., Girod A., Bossemeyer D.,  
 RA Kinzel V.;  
 RT "Intracellular distribution of mammalian protein kinase A catalytic  
 RT subunit altered by conserved Asn2 deamidation.";  
 RL J. Cell Biol. 148:715-726(2000).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) IN COMPLEX WITH PKIA.  
 RX MEDLINE=93193878; PubMed=8443157;  
 RA Zheng J., Knighon D.R., ten Eyck L.F., Karlsson R., Xuong N.,  
 RA Taylor S.S., Sowadski J.M.;  
 RT "Crystal structure of the catalytic subunit of cAMP-dependent protein









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CC EMBL; AY083469; AAM00022.1; -.
CC PIR; C32571; C32571.
CC PIR; S30504; S30504.
CC HSSP; Q63450; 1A06.
CC MGD; MGI:104557; Rps6ka3.
CC GO; GO:004674; F:protein serine/threonine kinase activity; IDA.
CC InterPro; IPR000961; Pkinase.C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 2.
CC Pfam; PF00433; pkinase.C; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 2.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TK; 2.
CC SMART; SM00219; TyRK; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 2.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 2.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 2.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding; Repeat; Multigene family; Phosphorylation.
KW DOMAIN 68 327 PROTEIN_KINASE_1.
FT FT BIND 74 82 ATP (BY SIMILARITY).
FT BINDING 100 100 ATP (BY SIMILARITY).
FT ACT_SITE 193 193 BY SIMILARITY.
FT NP_BIND 428 436 ATP (BY SIMILARITY).
FT BINDING 451 451 ATP (BY SIMILARITY).
FT ACT_SITE 539 539 BY SIMILARITY.
FT MOD_RES 227 227 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 365 365 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 369 369 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 386 386 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 577 577 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 737 737 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 740 AA; 83693 MW; 0CD54E5918567007 CRC64;

Query Match 23.8%; Score 501.5; DB 1; Length 740;
Best Local Similarity 35.1%; Pred. No. 5.4e-27;
Matches 110; Conservative 66; Mismatches 118; Indels 19; Gaps 7;

Qy 11 VFDEEDVNFDFEILRAIGKSGFGEVCIVOK---NDTKKMKAMKYNKQKCVNEVRN 67
Db 56 VKEGHEKADPQFELLKVLGQSGFGKFLVKISGSDARQIYAMKVLKATLKVRDVRT 115
Qy 68 VFKEQLINQGLEHPPFLVNLWYSFQDEEDMFVMDVLLGGDLRYHLQONVHPKBEVKLFI 127
Db 116 KM-ERDILVEVNHPPVIVKLVAFQTEGKVLILDPLRGGDLFTRLSKVMFTEDVDFYL 174
Qy 128 CELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDNIA-AMLPRETQITTWAGTKPY 186
Db 175 AELALALDHLHSLGLIYRDLAPENILLDEEGHKLTLDFGLSKESIDHEKKAYSFCGTVEY 234
Qy 187 MAPENFSRKGAGSFAVDWVSLGVTAYELLGRPRPYHRSSTSKETVHTFTTWTVPY 246
Db 235 MAPEVVRNR---GHTQSADWHSFGVLMFEMLTGTLFP---QOKDKETMTWLKAKLGMP 288
Qy 247 SAWQEMVSLKLLKLEPNPDQFSQ----LSDVQNFYPMNDINMDVAPQKRLIFGFIPTNK 302
Db 289 QFLSPEAQSLRLMLFKRNPANRLAGAPDGVVEIKRHSFFSTIDWKLVRREIHPFPKPAT 348
Qy 303 GR----LNCDDTF 311
Db 349 GRPDTFTYDFPEP 361

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RESULT 15
YPK2_YEAST
ID YPK2_YEAST STANDARD; PRT; 677 AA.
AC P18961;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase YPK2/YKR2 (EC 2.7.1.-).
OS YPK2 OR YKR2 OR YMR104C OR YMR718.03C.
GN Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89306654; PubMed=2663649;
RA Kubo K., Ohno S., Matsumoto S., Yahara I., Suzuki K.;
RT "A novel yeast gene coding for a putative protein kinase.";
RL Gene 76:177-180(1989).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=93173125; PubMed=8437590;
RA Chen P.C., Lee K.S., Levin D.E.;
RT "A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell growth in Saccharomyces cerevisiae.";
RL Mol. Gen. Genet. 236:443-447(1993).
[3]
RN SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jørgensen K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrall B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
RL Nature 387:90-93(1997).
CC -1- FUNCTION: Plays an essential role in the proliferation of yeast cells.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC RAC SUBFAMILY. STRONGEST TO YPK1.
-----
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EMBL; M24929; AAA78259.1; -.  
EMBL; Z49702; CAA89740.1; -.  
PIR; J50178; J50178.  
HSSP; P05132; 1CTP.  
GeneOnline; 142772; -.  
SGD; S0004710; YPK2.  
GO; GO:0005737; C:cytoplasm; IDA.  
GO; GO:0005634; C:nucleus; IDA.  
InterPro; IPR000961; Pkinase.C.  
InterPro; IPR000719; Prot\_kinase.  
InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
InterPro; IPR002290; Ser\_thr\_pkinase.  
Pfam; PF00069; pkinase; 1.  
Pfam; PF00433; pkinase.C; 1.  
ProDom; PD000001; Prot\_kinase; 1.  
SMART; SM00133; S\_TK\_X; 1.  
SMART; SM00220; S\_TK; 1.  
PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
Transferrase; Serine/threonine-protein kinase; ATP-binding.  
DOMAIN 35 57 HIS-RICH.  
DOMAIN 344 599 PROTEIN\_KINASE.



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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:46:29 ; Search time 21 Seconds  
(without alignments)  
1813.897 Million cell updates/sec

Title: US-10-667-442-2  
Perfect score: 2104  
Sequence: 1 MGNTSRKPPVDEEDVNF.....NLALQTKDPQGEDQNNNL 396

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query %	ID	Description
1	843.5	40.1	379	2 T23688	hypothetical prote
2	537	25.5	479	2 A38578	protein kinase 2 (
3	528.5	25.1	648	1 JQ1150	protein kinase (SC
4	521	24.8	480	2 S56639	ribosomal protein
5	516.5	24.5	465	2 S68462	protein kinase ATP
6	513	24.4	680	2 S37955	protein kinase YPK
7	511.5	24.3	696	2 S55694	protein kinase (SC
8	510.5	24.3	353	2 C31751	protein kinase (SC
9	508	24.1	471	2 S68463	protein kinase ATP
10	507	24.1	352	2 S19027	protein kinase A (
11	506.5	24.1	785	2 T20232	hypothetical prote
12	506	24.0	359	2 T21211	hypothetical prote
13	503	23.9	375	2 T21212	hypothetical prote
14	502.5	23.9	351	1 OKHYCA	protein kinase (SC
15	502.5	23.9	823	2 A58986	probable protein k
16	501.5	23.8	360	1 OKHUCG	protein kinase (SC
17	501.5	23.8	740	2 I38556	ribosomal protein
18	501	23.8	677	2 JS0178	protein kinase YKR
19	500.5	23.8	733	2 A57459	ribosomal protein
20	499	23.7	359	1 OKWCL1	protein kinase (SC
21	498.5	23.7	351	1 OKHUC2	protein kinase (SC
22	498.5	23.7	351	1 OKRT2C	protein kinase (SC
23	496.5	23.6	351	1 OKB02C	protein kinase (SC
24	496	23.6	351	1 OKRTCB	protein kinase (SC
25	496	23.6	351	1 OKMSCB	protein kinase (SC
26	496	23.6	351	1 OKHYCB	protein kinase (SC
27	496	23.6	352	2 S19028	protein kinase (SC
28	496	23.6	375	1 OKKWC2	protein kinase (SC
29	495.5	23.6	586	2 A53758	protein kinase C (

30	495.5	23.6	587	2 A49509	protein kinase C (
31	495.5	23.6	689	1 A53791	beta-adrenergic-re
32	494.5	23.5	752	1 A32571	ribosomal protein
33	493.5	23.5	352	2 JC7968	cyclic adenosine 3
34	493.5	23.5	398	1 OKBYC3	probable serine/th
35	493.5	23.5	646	2 T38171	protein kinase (SC
36	493.5	23.5	689	1 A40088	beta-adrenergic-re
37	492.5	23.4	351	1 OKMSCA	protein kinase (SC
38	492.5	23.4	689	1 I56531	beta-adrenergic-re
39	492.5	23.4	1102	2 T28666	protein kinase C-r
40	491.5	23.4	733	1 B30001	ribosomal protein
41	490	23.3	334	2 A60543	protein kinase (SC
42	490	23.3	512	2 A54000	protein kinase (SC
43	488.5	23.2	629	2 A30001	ribosomal protein
44	487	23.1	380	1 OKBYC2	protein kinase (SC
45	486.5	23.1	351	1 OKHUCB	protein kinase (SC

## ALIGNMENTS

### RESULT 1

T23688  
hypothetical protein M03C11.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T23688  
R:McMurray, A.  
submitted to the EMBL Data Library, April 1995  
A:Reference number: Z19783  
A:Accession: T23688  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-379 <WILL>  
A:Cross-references: EMBL:Z49128; PIDN:CAA88953.1; GSPDB:GN00021; CESP:M03C11.1  
A:Experimental source: clone M03C11  
C:Genetics:  
A:Gene: CESP:M03C11.1  
A:Map position: 3  
A:Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3  
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match	40.1%;	Score	843.5;	DB 2;	Length	379;			
Best Local Similarity	44.1%;	Pred. No.	5.7e-31;						
Matches	158;	Conservative	70;	Mismatches	117;	Indels	13;	Gaps	4;
QY	22	HFEILRAIGKSGFGEVCIVQKNDTKQCMATKMKQKCVERNVNFVKELQIMQGLEHP	81						
DB	27	HFSVIRSIGRGAFGKVCIVQBRKTKKYPALKYMKRRCIEKGVAANVIRELTLLSKMHP	86						
QY	82	FLVNLWYSQDSQSEDMFVVDLLGGDLRYHLQONVHPKSEETVKLPICSLVMDLYLQNR	141						
DB	87	FIVNLWYTFQGDYMYMVSDLLGGDLRYHLSSQKQKPAEDRAKLYLCICLAVEYLNEMK	146						
QY	142	IIHRDKPDNILLDSHGHHVHTDFNIAAMLPRETOITTMAGTKPYMAPFESS--RKAG	199						
DB	147	IVHRDIKPENILDSQGHALTDLNLAQLQEDDQLATSYSGTRPYMAPEIATYLEIEDG	206						
QY	200	YSPAVDWNSLGTAYELLGRPHIRSRSTSSKEIVHTFETVTVTPYPMASQEMVSLKK	259						
DB	207	YDSRYDWMALGVCFYEMLRGRTPPEFSRTPPEEAYAFRESSIPYPAHWPDTLLQFINS	266						
QY	260	LLEPNPDORFQSLSDVQNFPMYNDINWDAVFKRLIPGFIPNKGRLNCDPTPELEEMILE	319						
DB	267	MLKPKKRLVGLKAIKHSYTERIDPKSVPEKKSPVFIPECKGLNCDPMYELSERILV	326						
QY	320	SKPLHKKKKRLAKKEKMKRCKDSSQTCLLQEHLDVQKEFTIFNREKVNDRDNFKQPN	377						
DB	327	STPIH--RRRTNHNNSGRSSSEPQNAALVE---VSKAFIDFSRHV-----KIEPN	373						

### RESULT 2

A38578

protein kinase 2 (EC 2.7.1.1) - slime mold (Dictyostelium discoideum)  
C;Species: Dictyostelium discoideum  
C;Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 24-Sep-1999  
C;Accession: A38578  
R;Haribabu, B.; Dottin, R.P.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991  
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum  
A;Reference number: A38578; MUID:91142122; PMID:1996312  
A;Accession: A38578  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <HAR>  
A;Cross-references: GB:M59744; NID:gl67717; PID:AAA33186.1; PID:gl67718  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine  
F;151-407/Domain: protein kinase homology <KIN>  
F;159-167/Region: protein kinase ATP-binding motif

Query Match 25.5%; Score 537; DB 2; Length 479;  
Best Local Similarity 36.2%; Pred. No. 2.4e-17;  
Matches 117; Conservative 66; Mismatches 124; Indels 16; Gaps 6;

Qy 11 VFDEN-EDVNFDPHEILRAIGKSGFGEVCIYQKNDTKKMCAMKMKQKVERNEVRNF 69  
Db 140 IFSKNQKQATKDDPELLNVIGKSGFGKVMQVKKGGEDKIPAMKVLKDAIIARKQVNHK 199  
Qy 70 KELOIMQGLEHPPFLVNIWYFQDEDMFVVDLLGLDRLYLHQQNVHFKETVKLF 129  
Db 200 SEKITLQCSHPFTVNIHAYFQTKLYMVLDFVNGELFFHLKRGFPSEPRKTYAAE 259  
Qy 130 LVMAIDYLOQRITHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTMAGTKPYMAP 189  
Db 260 IVSALDHLKQDIVRDLKPNILLDEGHICITDFGLSKKIETDTGTFCTGTPVLAP 319  
Qy 190 EMPSSRKAGYSPAVDWSLGVYAYELLRGRPHYHRSSTSSKEIVHTPTVTVVYPSAW 249  
Db 320 EVLN---GHGHCADVMSLGLTLLYEMLTGLPPYSQNVSTMVQKILNGELKIPTY---I 373  
Qy 250 SQENVSLKLLKLEPNPQRSOL---SDVQNPVYNDINWDVAFQKRLIPGPIP-----NKG 303  
Db 374 SPEAKSLLEGLLTREVDRKLTGKGGEVQKHPWPKNIDWKLDRKVEVHFQKPKVSGTD 433  
Qy 304 RLNCDDPTFELE---EMILESPL 323  
Db 434 ISQIDPVFTQBRPMSLVEISAL 456

RESULT 3  
JQ1150  
protein kinase (EC 2.7.1.37) cAMP-dependent, catalytic chain - slime mold (Dictyostelium  
C;Species: Dictyostelium discoideum  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 24-Apr-1998  
C;Accession: JQ1150  
R;Buerki, E.; Anjard, C.; Scholder, J.C.; Raymond, C.D.  
Gene 102, 57-65, 1991  
A;Title: Isolation of two genes encoding putative protein kinases regulated during Dicty  
A;Reference number: JQ1150; MUID:91323730; PMID:1864510  
A;Accession: JQ1150  
A;Molecule type: DNA  
A;Residues: 1-648 <BUE>  
A;Cross-references: GB:M38703  
C;Genetics:  
A;Gene: PK2  
A;Introns: 578/3  
C;Complex: heterodimer with regulatory chain; active catalytic chain is released when ch  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Note: important for cell type differentiation and fruiting body morphogenesis  
C;Superfamily: Dictyostelium cAMP-dependent protein kinase catalytic chain; protein kin  
C;Keywords: ATP; magnesium; phosphoprotein; phosphotransferase; serine/threonine-specifi  
F;126-223/Region: glutamine-rich  
F;297-312/Region: glutamine-rich  
F;334-590/Domain: protein kinase homology <KIN>

F;342-350/Region: protein kinase ATP-binding motif  
C;Species: Dictyostelium discoideum  
C;Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 24-Sep-1999  
C;Accession: A38578  
R;Haribabu, B.; Dottin, R.P.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991  
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum  
A;Reference number: A38578; MUID:91142122; PMID:1996312  
A;Accession: A38578  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <HAR>  
A;Cross-references: GB:M59744; NID:gl67717; PID:AAA33186.1; PID:gl67718  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine  
F;151-407/Domain: protein kinase homology <KIN>  
F;159-167/Region: protein kinase ATP-binding motif

Query Match 25.1%; Score 528.5; DB 1; Length 648;  
Best Local Similarity 34.2%; Pred. No. 7.5e-17;  
Matches 110; Conservative 76; Mismatches 115; Indels 21; Gaps 8;

Qy 9 PPVFDENEDVNFDPHEILRAIGKSGFGEVCIYQKNDTKKMC--AMKMKQKQKVERNEVR 66  
Db 325 PPV---NARERLKEPKQIRVLGTGTFGKVVLIQ--NTKDGCCYAMKCLNKAAYVQVKVE 379  
Qy 67 NYVEKLOIMQGLEHPPFLVNIWYFQDEDMFVVDLLGLDRLYLHQQNVHFKETVKLF 126  
Db 380 HLNSEKSLISSHHPFVNIWYFQDEDMFVVDLLGLDRLYLHQQNVHFKETVKLF 439  
Qy 127 ICENVMAIDYLOQRITHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTMAGTKPY 186  
Db 440 AAEIVLALFELHKQINIVRDLKPNILLDQGHKIKITDFGAKRV--EDRTFTLCGTPEY 497  
Qy 187 MAPENPSSRKAGYSPAVDWSLGVYAYELLRGRPHYHRSSTSSKEIVHTPTVTVVYTP 246  
Db 498 LAPETIQSK---GHGKAVDWMALGILIFEMLAGYPPFY---DDTTPAIYNNKILAGRITPP 551  
Qy 247 SAMSQEMVSLKLLKLEPNPQRSOLS---DVQNPVYNDINWDVAFQKRLIPGPIPKN 302  
Db 552 LGFDVDAKDLIKRLLTADRTRILGALKDQALDVKRWFSDDINWELYQDRNGPFIPIKI 611  
Qy 303 RLNCDDPTFELE---EMILESPL 322  
Db 612 QHGDSSNPFMYDEBEMVEEP 633

RESULT 4  
S56639  
ribosomal protein S6 kinase homolog (clone AspK1) - oat  
N;Alternate names: mitogen-activated protein kinase pp70 homolog  
C;Species: Avena sativa (oat)  
C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 24-Sep-1999  
C;Accession: S56639  
R;Huttly, A.K.; Phillips, A.L.  
Plant Mol. Biol. 27, 1043-1052, 1995  
A;Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that  
A;Reference number: S56638; MUID:95284341; PMID:7766874  
A;Accession: S56639  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-480 <HUT>  
A;Cross-references: EMBL:X79992; NID:g871985; PID:CAA56313.1; PID:g871986  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom  
C;Keywords: ATP; phosphotransferase; protein kinase  
F;149-407/Domain: protein kinase homology <KIN>  
F;157-165/Region: protein kinase ATP-binding motif

Query Match 24.8%; Score 521; DB 2; Length 480;  
Best Local Similarity 35.3%; Pred. No. 1.2e-16;  
Matches 107; Conservative 62; Mismatches 124; Indels 10; Gaps 3;

Qy 14 ENEDVNFDPHEILRAIGKSGFGEVCIYQKNDTKKMCAMKMKQKVERNEVRNVPKELQ 73  
Db 142 ENEAVGLDNFVLEKLVGQGAFGKVVQYVRMKGTSSEIYAMKVMRKDKILEKHAHYMKAERD 201  
Qy 74 IMQGLEHPPFLVNIWYFQDEDMFVVDLLGLDRLYLHQQNVHFKETVKLFICBLVMA 133  
Db 202 ILTKVDHPFVQVRLYRFPQTKYRLYLVDVFNQGHLEFQLYQQGLFREELARIYTAELVSA 261  
Qy 134 LDYLOQRITHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTMAGTKPYMAPMFS 193  
Db 262 VAHLHANGIMHRLDKPENILLDARGHMLTDFGLAKEFDENTRSNCGCTVETWAPETV- 320  
Qy 194 SRKAGYSPAVDWSLGVYAYELLRGRPHYHRSSTSSKEIVHTPTVTVVYPSAWQEM 253  
Db 321 --QGRGHDKAADWMSVGIILLFEMLTGKPPPF---GGRNDKIQQKIVREKMKLPYSLSSEV 375

Qy 254 VSLIKLLLEPNPDORFSQ-----LSDVQVFPYMNNDINWDAVQKRLIPGFIPIKGRNLCDP 309  
 Db 376 HSLIKGLLHKAGKRLGSLGSGDEIKVHKWFKAVNKKRLERQIQSPFCFENVAGQTCTA 435  
 Qy 310 TFE 312  
 Db 436 NPD 438

## RESULT 5

S58462  
 A:Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein kinase ATPK6/ATPK1 (EC 2.7.1.1) - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 05-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 24-Sep-1999  
 C:Accession: S58462; A54141  
 R:Mioguchi, T.; Hayaashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K. FEBS Lett. 358, 199-204, 1995  
 A:Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold  
 A:Reference number: S58462; MUID:95129712; PMID:7828736  
 A:Accession: S58462  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-465 <MIZ>  
 A:Cross-references: EMBL:D42056; NID:9867996; PIDN:BAA07656.1; PID:d1008238; PID:g867997  
 R:Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.  
 J. Biol. Chem. 269, 17586-17592, 1994  
 A:Title: apk1, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation, characterization, and expression  
 A:Reference number: A54141; MUID:94292519; PMID:7912697  
 A:Contents: ecotype Landsberg erecta  
 A:Accession: A54141  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-465 <ZHA>  
 A:Cross-references: GB:L29030; NID:9508307; PIDN:AAA21142.1; PID:9508308  
 A:Note: sequence extracted from NCBI backbone (NCBIN:149344, NCBIIP:149415)  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
 F:132-389/Domain: protein kinase homolog <KIN>  
 F:140-148/Region: protein kinase ATP-binding motif

Query Match 24.5%; Score 516.5; DB 2; Length 465;  
 Best Local Similarity 34.1%; Pred. No. 1.9e-16;  
 Matches 102; Conservative 66; Mismatches 120; Indels 11; Gaps 3;  
 Qy 18 VNFDFEILRAIGKSGFGEVCIQKNDTKCMKMYKQKCKVERNEVNFKEIQMG 77  
 Db 129 VGIDDFEYMKVVGKAFKQYQVRKKTSEIYAMKVRKDHIMEKNHAEYMKARDIILTK 188  
 Qy 78 LEHPFLVNLVYSFQDEEDMFVVDLLGGDLRYHLQQNVHPKSETVKLPICELVMDLYL 137  
 Db 189 IDHPFIVQLKYSFQTKRYLYLVDFINGHLLFFQYHOGLFREDLARTVTAIVSAVSHL 248  
 Qy 138 QNQRITHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTMAGTKPYMAPEMSSRK 197  
 Db 249 HEKGIMHRLKPEINLMDTGHWLTDGFLAKEPEENTRSNMCQTEYMAPEIV--RG 305  
 Qy 198 AGYSFADVMSLGVATAYELLRRRYPYHRSSTSSKEIVHTPTVTVTYPSAWSQMWGLL 257  
 Db 306 KGHDKAADVMSVGIILLYEMLTGKPPFLGSKGIQKIV----KDKIKLPQFLSNEAHAIL 361  
 Qy 258 KKLEPNPDOR----PSQLSDVQNFYMNNDINWDAVQKRLIPGFIPIKGRNLCDPTE 312  
 Db 362 KGLLQKEPERRLGSGLSGABEIKQHKWFKGINWKKLEAREVMPSPKPEVSGQCINFD 420

## RESULT 6

S37955  
 A:Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein kinase YPK1 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 24-Sep-1999  
 C:Accession: S37955; A31248; S30903

R:Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P. submitted to the Protein Sequence Database, March 1994  
 A:Reference number: S37955  
 A:Accession: S37955  
 A:Molecule type: DNA  
 A:Residues: 1-680 <RAM>  
 A:Cross-references: EMBL:Z28126; NID:g486212; PIDN:CAA81967.1; PID:g486213; MIPS:YKL12  
 A:Experimental source: strain S288C  
 R:Maurer, R.A.  
 DNA 7, 469-474, 1988

A:Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein kinase YPK1 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)  
 A:Reference number: A31248; MUID:89090805; PMID:2850145

A:Accession: A31248  
 A:Molecule type: DNA  
 A:Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>  
 A:Cross-references: EMBL:M21307; NID:g172180; PIDN:AAA34880.1; PID:g172181  
 R:Chen, P.; Lee, K.S.; Levin, D.E.  
 Mol. Gen. Genet. 236, 443-447, 1993

A:Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell growth in *Saccharomyces cerevisiae*

A:Reference number: S30903; MUID:93173125; PMID:8437590  
 A:Accession: S30903  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>

C:Genetics:  
 A:Gene: SGD:YPK1  
 A:Cross-references: SGD:S0001609; MIPS:YKL126W  
 A:Map position: 11L  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
 F:345-602/Domain: protein kinase homolog <KIN>  
 F:353-361/Region: protein kinase ATP-binding motif  
 F:470/Active site: Asp #status predicted

Query Match 24.4%; Score 513; DB 2; Length 680;  
 Best Local Similarity 32.0%; Pred. No. 3.8e-16;  
 Matches 115; Conservative 78; Mismatches 124; Indels 42; Gaps 10;

Qy 8 KPVPFEDENVDNDFHILRAIGKSGFGEVCIQKNDTKCMKMYKQKCKVERNEVNF 67  
 Db 335 KP-----SRNKPLSIDDFLLKVIKSGFQKQVQKQKQTKQYALKAKRKSVISKSEVTH 391  
 Qy 68 VFKELOMQGLHEHFLVNLVYSFQDEEDMFVVDLLGGDLRYHLQQNVHPKSETVKLFI 127  
 Db 392 TLARTVLRVDCFPVPLKESFQSPKLYVFLAFINGGELFYHLQKSGRFDLSRPFYT 451  
 Qy 128 CELVMDLYQNRQRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQIT-TMAGTKPY 186  
 Db 452 AELLCALDNLHLKDVVYRDLKPEINLLDYQGHIALCDFGLCKLNKKDDDKTDFCGTPEY 511  
 Qy 187 MAPEMFSSRKAGYSPADVMSLGVATAYELLRRRYPYHRSSTSSKEIVHTFTTV--V 243  
 Db 512 LAPELL---LGLGYTKAVDMMTLGLVLYEMUTGLPPYY-----DEDVPMYKKILQEP 562  
 Qy 244 TYPAWSQEMVSLKCLLEPNPDOR--FSQLSDVQNFYMNNDINWDAVQKRLIPGFI 301  
 Db 563 VPDGFDKADKLLIGLLSRDPTRELGVNGADEIRNHFPFSLQSKRLMKGYIPPKPA 622  
 Qy 302 KGRNLCDPTELEEMILESKPLHKKKRLAKGKDMKCDSSQTCLLQEHLL-DSVQKEF 359  
 Db 623 VS--NSMDTSNDFBEFTREKPI-----DS-----VVDYLSESVQKQF 658

## RESULT 7

S55694  
 A:Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein kinase YPK1 (EC 2.7.1.37) sck1, cAMP-dependent - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C>Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Nov-2000  
 C:Accession: S55694; T38040  
 R:Jin, M.; Fujita, M.; Culley, B.M.; Apolinario, E.; Yamamoto, M.; Maundrell, K.; Hoff  
 Genetics 140, 457-467, 1995  
 A:Title: sck1, a high copy number suppressor of defects in the cAMP-dependent protein kinase  
 A:Reference number: S55694; MUID:96120227; PMID:7498728





Db 116 PFGNDTDSKSPBESVGVGIEDPEVLKVVQGAFGKVVQVRKDTSEIVAMKVMRKDK 175  
QY 59 CVERNEVNFKELOIMOGLHPPFLVNLWYSFQDEDMFVVDLLGGDLHYHLQONVHP 118  
Db 176 IVEKNHABYMKAEKIDILKIDHPFVQLKYSFQTKYRLYLVDLDFNGHLPFLQYHGLF 235  
QY 119 KEETVKLPICELVMAIDYQONRIIHRDKPDNILLDEGHVHITDFNIAAMLPRETOIT 178  
Db 236 REDLARVTAETVSVVSHLHEKIMHRLDKPENILMDVDGHWMLTDFGLAKEFEENTSN 295  
QY 179 TWAGTKPNMPEMPSRRKAGSVFVDMWSLGVTAAYELLGRPPVHRSSTSSKEIVHTF 238  
Db 236 SMCCTETMAPEIV---RGKGDHKAADWWSGILLYEMLTGKPPPLGSKGKIQQKIV--- 349  
QY 239 ETTVVTVPSAWSQEMVSLKLLKLEPNPDORF---SQLSDVQNPFPYMDINDWAVFQRL 294  
Db 350 -KDKIKLQFVFNENAHLLKGLLQKEPERRLGSGPGEAEIKKHGFKAINWKKLEAREV 408  
QY 295 IPGFIPNKRGLNCDPTFE 312  
Db 409 QPSFKPAVSGRQCIANFD 426

## RESULT 10

S19027  
protein kinase A (EC 2.7.1.1) catalytic chain - California sea hare  
C:Species: Aplysia californica (California sea hare)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Jun-1999  
C:Accession: S19027  
R:Beushausen, S.; Bergold, P.; Sturmer, S.; Elste, A.; Roytenberg, V.; Schwartz, J.H.; H  
Neuron 1, 853-864, 1998  
A:Title: Two catalytic subunits of cAMP-dependent protein kinase generated by alternativ  
A:Reference number: S19027; MUID:90166564; PMID:2483106  
A:Accession: S19027  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-352 <BEU>  
A:Cross-references: EMBL:X63420; NID:g5576; PIDN:CAA45014.1; PID:g5577  
A>Note: the authors translated the codon AAC for residue 29 as Asp, GAC for residue 45 a  
as Glu, CTA for residue 271 as Glu, AAC for residue 285 as Asp, and AAC for residue 288  
C:Superfamily: kinase-related transforming protein; protein kinase homology  
C:Keywords: phosphotransferase  
F:42-299/Domain: protein kinase homology <KIN>

Query Match 24.1%; Score 507; DB 2; Length 352;  
Best Local Similarity 33.3%; Pred. No. 4e-16;  
Matches 108; Conservative 82; Mismatches 104; Indels 30; Gaps 10;

QY 21 DHFEILRAIGKSGFGEVCIVQ-KNDTKMKCAMKYNKQKVERNEVRNVFKELQIMOGL 79  
Db 42 DDFDRIKLTGSGFGRVLMVQHKGSRNFYAMKILDKQVVKLQVHTLNEKKILQIN 101  
QY 80 HPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHPKETVKLFICELVMAIDYQON 139  
Db 102 FPFVLKLEYSFKDNLVYLFVVTGEMFSLHRLRIGRFSFPHSRFYAAQIVLVLEYLH 161  
QY 140 QRIIHRDKPDNILLDEGHVHITDFNIAAMLPRETOITTWAGTKPNMPEMPSRRKAG 199  
Db 162 LDIMYRDLKPNLLSDSYGLKVTDFGFAKRVKGT--WTLGCTPEYLAPLILSK---G 216  
QY 200 YSFVDMWSLGVTAAYELLGRPPVHRSSTSSKEIVHTFETV---VTPSAWSQEMVSL 256  
Db 217 YNKAVDMWALGVLIYEMAGYPPFP-----ADQPIYIEKIVSGKVFSPHFSDDLKDL 270  
QY 257 LKKLLEPNPDORFSQL-----SDVQNPFPYMDINDWAVFQRLIPGFIIP-NKGRNLCDPTF 311  
Db 271 LKNLLQVLDLTKRFGNLKNGVNDIKHKNFSTTDITAIYQKRVAPFPVPTKRG---AGDTA 327  
QY 312 ELEEMILESPLHKKKKLAKKEK 335  
Db 328 NFDD---YEEEPD-----RISSTEK 344

## RESULT 11

T20232  
hypothetical protein C54G4.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T20232  
R:Wilkinson, J.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19241  
A:Accession: T20232  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-785 <WIL>  
A:Cross-references: EMBL:Z75533; PIDN:CAA99814.1; GSPDB:GN00019; CESP:C54G4.1  
A:Experimental source: clone C54G4  
C:Genetics:  
A:Gene: CESP:C54G4.1  
A:Map position: 1  
A:Introns: 55/3; 188/2; 237/2; 339/3; 397/2; 474/3; 504/3; 558/2; 594/3; 687/1; 736/2  
C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology

Query Match 24.1%; Score 506.5; DB 2; Length 785;  
Best Local Similarity 36.3%; Pred. No. 8.4e-16;  
Matches 109; Conservative 73; Mismatches 107; Indels 11; Gaps 8;

QY 14 ENEDVNFDPHEILRAIGKSGFGEVCIVQK---NDTKMKCAMKYNKQKVERNE-VRNVF 69  
Db 8 EGEKVSMEINFAILLVGLGKYGKVFVLRKVGKDDNTIYAMKVRTRVLTKQKTLHTM 67  
QY 70 KELQIMOGLS-HPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHPKBTYVQLFIC 128  
Db 68 AERQVLERLGRTPFLVNLVYAFQDTDKLHIVMEVYRGELFTLHCSRGHFDEAARFVIA 127  
QY 129 ELVWALDYQONRIIHRDKPDNILLDEGHVHITDFNIAAM-LPRE-TQITTWAGTKPY 186  
Db 128 ELVVAIDSLHQKVIYRDLKLENILLDEEGHVKLTDFGLSKLFLPGLDRANSYCGTIEY 187  
QY 187 MAPMPSRRKAGSVFVDMWSLGVTAAYELLGRPPVHI-RSSTSSKEIVHTFETTVVTV 245  
Db 188 MSPEVINRPEG-GVSDVDMWSLGVISFELLTGSPTVDGAQNSKDKIAKRIIMTKKYPF 246  
QY 246 PSAWSQEMVSLKLLKLEPNPDQR--FSQLSDVQNPFPYMDINDWAVFQRLIPGFIIPNKG 303  
Db 247 PKTMDVDARDFIGQLLEKLEKRLGNGVDBIKHKNFSSIDMDAAVAKRTLKPVIVPRIG 306

## RESULT 12

T21211  
hypothetical protein ZK909.2a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T21211; T28100  
R:McLay, K.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19391  
A:Accession: T21211  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-359 <WIL>  
A:Cross-references: EMBL:Z81511; PIDN:CA04168.1; GSPDB:GN00019; CESP:ZK909.2a  
A:Experimental source: clone F21F12  
R:White, S.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z20469  
A:Accession: T28100  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-359 <W12>  
A:Cross-references: EMBL:Z82096; PIDN:CA05034.1; GSPDB:GN00019; CESP:ZK909.2a  
A:Experimental source: clone ZK909  
C:Genetics:  
A:Gene: CESP:ZK909.2a  
A:Map position: 1

QY	131	VMALDYLNQRIIHRDMKPDNILLDEGHVHITDENIAAMLPRETOITTTWAGTKPYMAPE	190
Db	160	VLAPEYTLASDLIYKDLKPEKNLLIDSTGYLKITDFGAKRVKGR--WTLCGTPPEYLAPE	217
QY	191	MFSSRKAGAGYSPAVDWSLGVATYELLGRRPYHRSSTSSKEIVHTFTTV---VTYPS	247
Db	218	IILSK---GYNKAVDWWALGVLIYEMAAGYPPPF-----ADQPIQIYEKIVSGKVFPS	268
QY	248	ANSQEMVSLKKLLEPNPDORSQ-----SDVQNPFYMNIDNWDVAPQKELIQGFIKNG	303
Db	269	HESNELKOLLKLLQVLDLTKRYGNLKNGVADIKNHKWFSGSTWDIAYKQKITPPSP-SKG	327
QY	304	RLN 306	
Db	328	ESN 330	
RESULT 14			
ORHYA			
Protein kinase (EC 2.7.1.37), CAMP-dependent, alpha catalytic chain - Chinese h			
C:Species: Cricetulus griseus (Chinese hamster)			
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jun-1999			
C:Accession: B40384			
R:Howard, P.; Day, K.H.; Kim, K.E.; Richardson, J.; Thomas, J.; Abraham, I.; Fl			
J. Biol. Chem. 266, 10189-10195, 1991			
A:Title: Decreased catalytic subunit mRNA levels and altered catalytic subunit			
A:Reference number: A40384; MUID:91244783; PMID:1645343			
A:Accession: B40384			
A:Molecule type: mRNA			
A:Residues: 1-351 <HOW>			
A:Cross-references: GB:M63311; NID:g191174; PID:AAA37010.1; PID:g191175			
C:Comment: The inactive enzyme contains two regulatory chains and two catalytic			
C:Comment: Two types found in mammalian tissue are distinguished by having either type I			
C:Comment: Both alpha and beta catalytic chains are found in many tissues, with			
C:Function:			
C:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-			
C:Superfamily: Kinase-related transforming protein; protein kinase homology			
C:Keywords: ATP; blocked amino end; CAMP binding; heterotetramer; lipoprotein;			
F:2-351/Product: protein kinase, CAMP-dependent, alpha catalytic chain #status			
F:42-298/Domain: protein kinase homology <KIN>			
F:50-58/Region: protein kinase ATP-binding motif			
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted			
F:3/Modified site: aspartic acid (Ser) #status predicted			
F:11,339/Binding site: phosphate (Asn) #status predicted			
F:55,56,122,128,171,184/Binding site: Mg-ATP (Phe, Gly, Glu, Thr) #status			
F:73,92,167,169/Active site: Lys, Glu, Asp, Lys #status predicted			
F:172,185/Binding site: magnesium (Asn, Asp) #status predicted			
F:198/Binding site: phosphate (Thr) (covalent) #status predicted			
Query Match 23.9%; Score 502.5; DB 1; Length 351;			
Best Local Similarity 34.0%; Pred. No. 6.2e-16;			
Matches 99; Conservative 76; Mismatches 97; Indels 19; Gaps 6			
QY	21	DHPEILRAIKGSFGVEICIVQKNDTKGCAKMYNKQKCVNERVNRVFKELQIMQGLEH	80
Db	42	DHEDRIKTYLTGTSFGFGRVLMVHKHETGNHYANKILDKQVKVKKQJIEHTLNEKRILQAVNF	101
QY	81	PFLVNLWYSPQDEBPMVVDLLGGDLRLVHLQNVHFKEETVKLFTCELVMALDYLNQ	140
Db	102	PFLVKLEFPKDNLSNLYMVMVEYVGGEMPSHLRRIGRFSFPHARFYAAQIVLTPEYLSL	161
QY	141	RIIHRMKNPNILLDEGHVHITDENIAAMLPRETOITTTWAGTKPYMAPESFSRKAGY	200
Db	162	DLIYRDLKPNLLIDQGYIQVDFGAKRVKGR--WTLCGTPPEYLAPEIILSK---GY	216
QY	201	SFPAVDWSLGVATYELLGRRPYHRSSTSSKEIVHTFTTV---VTYPSANQEMVSL	257
Db	217	NKAVDWWALGVLIYEMAAGYPPPF-----ADQPIQIYEKIVSGKRVFSPFSDDLKLL	270
QY	258	KLLEPNPDORSQ-----SDVQNPFYMNIDNWDVAPQKELIQGFIKNG	303
Db	271	RNLQVLDLTKRFGNLKNGVNDIKNHKWFATDWTDAITQKVEAPFIPKFKF	321



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:50:15 ; Search time 48 Seconds  
(without alignments)  
2329.088 Million cell updates/sec

Title: US-10-667-442-2  
Perfect score: 2104  
Sequence: 1 MGNATSRKPPVDFENEDVNF.....NLALEQTKDQGEDQNNL 396

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	100.0	396	9	US-09-801-876B-2
2	2104	100.0	396	12	US-10-667-442-2
3	2104	100.0	396	14	US-10-254-869-2
4	2089	99.3	396	9	US-09-841-683-11
5	2089	99.3	396	12	US-10-362-892-20
6	2089	99.3	396	12	US-10-182-243-33
7	2089	99.3	396	15	US-10-288-798-20
8	2083	99.0	396	15	US-10-410-764-101
9	2047	97.3	407	9	US-09-841-683-9
10	1814	86.2	358	15	US-10-108-260A-2674
11	1437.5	68.3	414	15	US-10-074-978A-158
12	1427	67.8	404	9	US-09-801-876B-4
13	1427	67.8	404	14	US-10-667-442-4
14	1427	67.8	404	14	US-10-254-869-4
15	1425.5	67.8	403	9	US-09-801-876B-5

16	1425.5	67.8	403	12	US-10-667-442-5	Sequence 5, Appli
17	1425.5	67.8	403	14	US-10-254-869-5	Sequence 5, Appli
18	1425.5	67.8	414	14	US-10-354-358-36	Sequence 36, Appl
19	1425.5	67.8	414	15	US-10-074-978A-157	Sequence 157, App
20	1324	62.9	419	9	US-09-799-875-14	Sequence 14, Appl
21	1324	62.9	419	12	US-10-649-156-14	Sequence 14, Appl
22	1324	62.9	419	14	US-10-303-664A-6	Sequence 6, Appli
23	1318	62.6	485	12	US-10-415-011-12	Sequence 12, Appl
24	1317.5	62.6	384	9	US-09-801-876B-6	Sequence 6, Appli
25	1317.5	62.6	384	12	US-10-667-442-6	Sequence 6, Appli
26	1317.5	62.6	384	14	US-10-254-869-6	Sequence 154, App
27	1317.5	62.6	488	15	US-10-074-978A-154	Sequence 18, Appl
28	1302	61.9	488	15	US-10-074-978A-18	Sequence 4, Appli
29	1278.5	60.8	399	10	US-09-819-607-4	Sequence 4, Appli
30	1278.5	60.8	399	12	US-10-633-631-4	Sequence 4, Appli
31	1259.5	59.9	375	12	US-10-168-582-12	Sequence 12, Appl
32	1201.5	57.1	364	12	US-10-206-915-572	Sequence 572, App
33	1201.5	57.1	364	12	US-10-199-670-572	Sequence 572, App
34	1201.5	57.1	364	12	US-10-201-858-572	Sequence 572, App
35	1201.5	57.1	364	12	US-10-205-890-572	Sequence 572, App
36	1201.5	57.1	364	12	US-10-208-024-572	Sequence 572, App
37	1201.5	57.1	364	12	US-10-201-853-572	Sequence 572, App
38	1201.5	57.1	364	12	US-10-174-581-572	Sequence 572, App
39	1201.5	57.1	364	12	US-10-176-483-572	Sequence 572, App
40	1201.5	57.1	364	12	US-10-176-749-572	Sequence 572, App
41	1201.5	57.1	364	12	US-10-176-914-572	Sequence 572, App
42	1201.5	57.1	364	12	US-10-176-915-572	Sequence 572, App
43	1201.5	57.1	364	12	US-10-176-484-572	Sequence 572, App
44	1201.5	57.1	364	12	US-10-180-550-572	Sequence 572, App
45	1201.5	57.1	364	12	US-10-183-014-572	Sequence 572, App

ALIGNMENTS

RESULT 1

US-09-801-876B-2  
; Sequence 2, Application US/09801876B  
; Patent No. US20020127683A1  
; GENERAL INFORMATION:  
; APPLICANT: YB, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160  
; CURRENT APPLICATION NUMBER: US/09/801,876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Human  
US-09-801-876B-2

Query Match	100.0%	Score 2104	DB 9	Length 396
Best Local Similarity	100.0%	Pred. No. 5e-169		
Matches	396	Conservative 0	Mismatches 0	Indels 0
				Gaps 0
QY	1	MGNATSRKPPVDFENEDVNFDFEILRAIGKSGFGEVCIVQKNVDTKGMCAKMTNKKCV	60	
DB	1	MGNATSRKPPVDFENEDVNFDFEILRAIGKSGFGEVCIVQKNVDTKGMCAKMTNKKCV	60	
QY	61	ERNEVRNFKELQIQGLEHPELVNLWYSFQDEDMFWVDLLGDLVHLQONVHKE	120	
DB	61	ERNEVRNFKELQIQGLEHPELVNLWYSFQDEDMFWVDLLGDLVHLQONVHKE	120	
QY	121	ETVKLFICELVNDYLNQRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETOITM	180	
DB	121	ETVKLFICELVNDYLNQRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETOITM	180	
QY	181	ACTKPYAMPFSSRRKAGYSPADWWSIGVTAYELLRGRPHIRSSSSKEIVTFT	240	

Db 181 AGTKPYMAPENFSSRGAGYSFAVDWNSLGTAYELLGRPPHYHRSSTSSKEIVHTFET 240  
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINNDVAFQKLLIPGFIP 300  
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINNDVAFQKLLIPGFIP 300  
Qy 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQTCLLQEHLDVQKEFI 360  
Db 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQTCLLQEHLDVQKEFI 360  
Qy 361 IFNREKVNDRDNFKQPNLALQTKDPOGEDQNNNL 396  
Db 361 IFNREKVNDRDNFKQPNLALQTKDPOGEDQNNNL 396

## RESULT 2

US-10-667-442-2  
; Sequence 2, Application US/10667442  
; Publication No. US20040043466A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160DIV II  
; CURRENT APPLICATION NUMBER: US/10/667,442  
; CURRENT FILING DATE: 2003-09-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-667-442-2

Query Match 100.0%; Score 2104; DB 12; Length 396;  
Best Local Similarity 100.0%; Pred. No. 5e-169;  
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGANTSRRKPPVFDENEDVNFDPHEILRAIGKSGFGEVCIVQKNDTKKCMKMYNNKQCV 60  
Db 1 MGANTSRRKPPVFDENEDVNFDPHEILRAIGKSGFGEVCIVQKNDTKKCMKMYNNKQCV 60  
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
Qy 181 AGTKPYMAPENFSSRGAGYSFAVDWNSLGTAYELLGRPPHYHRSSTSSKEIVHTFET 240  
Db 181 AGTKPYMAPENFSSRGAGYSFAVDWNSLGTAYELLGRPPHYHRSSTSSKEIVHTFET 240  
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINNDVAFQKLLIPGFIP 300  
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINNDVAFQKLLIPGFIP 300  
Qy 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQTCLLQEHLDVQKEFI 360  
Db 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQTCLLQEHLDVQKEFI 360  
Qy 361 IFNREKVNDRDNFKQPNLALQTKDPOGEDQNNNL 396  
Db 361 IFNREKVNDRDNFKQPNLALQTKDPOGEDQNNNL 396

## RESULT 3

US-10-254-869-2  
; Sequence 2, Application US/10254869  
; Publication No. US20030027307A1  
; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160DIV  
; CURRENT APPLICATION NUMBER: US/10/254,869  
; CURRENT FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Human  
US-10-254-869-2

Query Match 100.0%; Score 2104; DB 14; Length 396;  
Best Local Similarity 100.0%; Pred. No. 5e-169;  
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MGANTSRRKPPVFDENEDVNFDPHEILRAIGKSGFGEVCIVQKNDTKKCMKMYNNKQCV 60  
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
Qy 181 AGTKPYMAPENFSSRGAGYSFAVDWNSLGTAYELLGRPPHYHRSSTSSKEIVHTFET 240  
Db 181 AGTKPYMAPENFSSRGAGYSFAVDWNSLGTAYELLGRPPHYHRSSTSSKEIVHTFET 240  
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINNDVAFQKLLIPGFIP 300  
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMDINNDVAFQKLLIPGFIP 300  
Qy 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQTCLLQEHLDVQKEFI 360  
Db 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQTCLLQEHLDVQKEFI 360  
Qy 361 IFNREKVNDRDNFKQPNLALQTKDPOGEDQNNNL 396  
Db 361 IFNREKVNDRDNFKQPNLALQTKDPOGEDQNNNL 396

## RESULT 4

US-09-841-683-11  
; Sequence 11, Application US/09841683  
; Patent No. US20020081600A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomnichy, Boris  
; APPLICANT: Wang, Xiaoming  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Waikie, D. Wade  
; TITLE OF INVENTION: No. US20020081600A1 Human Kinase Proteins and Polynucleotide  
; FILE REFERENCE: LEX-0167-USA  
; CURRENT APPLICATION NUMBER: US/09/841,683  
; CURRENT FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: US 60/199,499  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 60/201,227  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: homo sapiens

US-09-841-683-11

Query Match 99.3%; Score 2089; DB 9; Length 396;  
Best Local Similarity 99.5%; Pred. No. 9.3e-168;  
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60  
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120  
DB 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120  
QY 121 ETVKLPICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETOITTM 180  
DB 121 ETVKLPICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETOITTM 180  
QY 181 AGTKPYMAPEMFSSRKAGYSFVDMWSLGVTAELLRGRPPYHRSSTSSKEIVHTPET 240  
DB 181 AGTKPYMAPEMFSSRKAGYSFVDMWSLGVTAELLRGRPPYHRSSTSSKEIVHTPET 240  
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNPFPYMDINWDVAFQKRLIPGP 300  
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNPFPYMDINWDVAFQKRLIPGP 300  
QY 301 NGRNLCDPTPELEEMILESPLHKKKXKLAKKXKMDKCDSSQTCLLQEHLDVQKEFI 360  
DB 301 NGRNLCDPTPELEEMILESPLHKKKXKLAKKXKMDKCDSSQTCLLQEHLDVQKEFI 360  
QY 361 IFNREKVRNDFNKRQPNLALBQTKDQGEDGQNNL 396  
DB 361 IFNREKVRNDFNKRQPNLALBQTKDQGEDGQNNL 396

## RESULT 5

US-10-362-892-20  
; Sequence 20, Application US/10362892  
; Publication No. US20040038881A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga  
; APPLICANT: NGUYEN, Daniel B.; WALIA, Narinder K.  
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.  
; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal  
; APPLICANT: DING, Li; PATTERSON, Chandra S.  
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.  
; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.  
; APPLICANT: ELLIOTT, Vicki S.; LU, Yan  
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.  
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda  
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.  
; APPLICANT: ZINGLER, Kurt A.; LU, Dyoung Aina M.  
; APPLICANT: LAL, Preeti G.; RAMKUMAR, Jayalaxmi  
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam  
; APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha  
; APPLICANT: BURFORD, Neil  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PP-0209 USN  
; CURRENT APPLICATION NUMBER: US/10/362,892  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: PCT/US01/27219  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,873  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US 60/231,357  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: US 60/232,654  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: US 60/234,902  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US 60/236,499  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/238,389

; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 60/240,542  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PERL Program  
; SEQ ID NO 20  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040038881A1 7946584CD1  
US-10-362-892-20

Query Match 99.3%; Score 2089; DB 12; Length 396;  
Best Local Similarity 99.5%; Pred. No. 9.3e-168;  
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYMKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120  
DB 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120  
QY 121 ETVKLPICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETOITTM 180  
DB 121 ETVKLPICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETOITTM 180  
QY 181 AGTKPYMAPEMFSSRKAGYSFVDMWSLGVTAELLRGRPPYHRSSTSSKEIVHTPET 240  
DB 181 AGTKPYMAPEMFSSRKAGYSFVDMWSLGVTAELLRGRPPYHRSSTSSKEIVHTPET 240  
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNPFPYMDINWDVAFQKRLIPGP 300  
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNPFPYMDINWDVAFQKRLIPGP 300  
QY 301 NGRNLCDPTPELEEMILESPLHKKKXKLAKKXKMDKCDSSQTCLLQEHLDVQKEFI 360  
DB 301 NGRNLCDPTPELEEMILESPLHKKKXKLAKKXKMDKCDSSQTCLLQEHLDVQKEFI 360  
QY 361 IFNREKVRNDFNKRQPNLALBQTKDQGEDGQNNL 396  
DB 361 IFNREKVRNDFNKRQPNLALBQTKDQGEDGQNNL 396

## RESULT 6

US-10-182-243-33  
; Sequence 33, Application US/10182243  
; Publication No. US20040048310A1  
; GENERAL INFORMATION:  
; APPLICANT: FLOWMAN, GREGORY D.  
; APPLICANT: WHYTE, DAVID  
; APPLICANT: MANNING, GERARD  
; APPLICANT: SUDARSANAM, SUCHA  
; APPLICANT: MARTINEZ, RICARDO  
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE  
; TITLE OF INVENTION: ENZYMS  
; FILE REFERENCE: 038602/1366  
; CURRENT APPLICATION NUMBER: US/10/182,243  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: PCT/US01/02337  
; PRIOR FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-182-243-33

Query Match 99.3%; Score 2089; DB 12; Length 396;

Best Local Similarity 99.5%; Pred. No. 9.3e-168;  
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKNKQCV 60  
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKNKQCV 60

Qy 61 ERNEVRNVFKELQIMOGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120  
Db 61 ERNEVRNVFKELQIMOGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120

Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180  
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180

Qy 181 AGTKPYMAPEMFSSRGAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240  
Db 181 AGTKPYMAPEMFSSRGAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDRFSQSDVQNFPPYNDINWDVAFQKRLIPGFI 300  
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDRFSQSDVQNFPPYNDINWDVAFQKRLIPGFI 300

Qy 301 NKGRINCDDPTFELEEMILESPLHKKKRLAKKCKDKMCKDSSQTCLOHLDVSVQKEFI 360  
Db 301 NKGRINCDDPTFELEEMILESPLHKKKRLAKKCKDKMCKDSSQTCLOHLDVSVQKEFI 360

Qy 361 IFNREKVNDRPNKQPNLALBQTKDPQGEDGQNNL 396  
Db 361 IFNREKVNDRPNKQPNLALBQTKDPQGEDGQNNL 396

## RESULT 7

US-10-288-798-20  
; Sequence 20, Application US/10288798  
; Publication No. US20030207299A1  
; GENERAL INFORMATION:  
; APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B.;  
; APPLICANT: WALIA, Narinder K.; HAPALIA, April J.A.;  
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;  
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;  
; APPLICANT: PATTERSON, Chandra; YUE, Henry;  
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;  
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;  
; APPLICANT: LU, Yan; ISON, Craig H.;  
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;  
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;  
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;  
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;  
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;  
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0209 USA  
; CURRENT APPLICATION NUMBER: US/10/288,798  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/27219  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/240,542  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US 60/238,389  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 60/236,499  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/234,902  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US 60/232,654  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: US 60/231,357  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: US 60/229,873  
; PRIOR FILING DATE: 2000-08-31  
; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PERL Program  
; SEQ ID NO 20  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030207299A1 7946584CD1  
US-10-288-798-20

Query Match 99.3%; Score 2089; DB 15; Length 396;  
Best Local Similarity 99.5%; Pred. No. 9.3e-168;  
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKNKQCV 60  
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKNKQCV 60

Qy 61 ERNEVRNVFKELQIMOGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120  
Db 61 ERNEVRNVFKELQIMOGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120

Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180  
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180

Qy 181 AGTKPYMAPEMFSSRGAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240  
Db 181 AGTKPYMAPEMFSSRGAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDRFSQSDVQNFPPYNDINWDVAFQKRLIPGFI 300  
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDRFSQSDVQNFPPYNDINWDVAFQKRLIPGFI 300

Qy 301 NKGRINCDDPTFELEEMILESPLHKKKRLAKKCKDKMCKDSSQTCLOHLDVSVQKEFI 360  
Db 301 NKGRINCDDPTFELEEMILESPLHKKKRLAKKCKDKMCKDSSQTCLOHLDVSVQKEFI 360

Qy 361 IFNREKVNDRPNKQPNLALBQTKDPQGEDGQNNL 396  
Db 361 IFNREKVNDRPNKQPNLALBQTKDPQGEDGQNNL 396

## RESULT 8

US-10-410-764-101  
; Sequence 101, Application US/10410764  
; Publication No. US20040005664A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Rudolph-Owen, Laura A.  
; APPLICANT: Welch, Nadine S.  
; APPLICANT: Olandt, Peter J.  
; APPLICANT: Tsai, Pong-Ying  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Carroll, Joseph M.  
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,  
; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,  
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MPI03-0520NMIM  
; CURRENT APPLICATION NUMBER: US/10/410,764  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: US 09/924,358  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/229,300  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: US 10/350,553  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: US 60/351,572  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: US 09/966,614





181 AGTKPYMAPEMFSSRRKAGYSFAVDWMSLGVTAAYELLRRGRRPYHRSSTSSKEIVHTFET 240  
 181 AGTKPYMAPEMFSSRRKAGYSFAVDWMSLGVTAAYELLRRGRRPYHRSSTSSKEIVHTFET 240  
 241 TTVTYSANSQEMVSLIKLLEPNPDRFSQSDVQNFYMDINNDVAFQKRLIPGFP 300  
 241 TTVTYSANSQEMVSLIKLLEPNPDRFSQSDVQNFYMDINNDVAFQKRLIPGFP 300  
 301 NGRNLCDPTFELEEMILESPLHKKKKRLAKKEKDMRKCDSSQ 344  
 301 NGRNLCDPTFELEEMILESPLHKKKKRLAKKEKDMRKCDSSQ 344

RESULT 11

US-10-074-978A-158  
 ; Sequence 158, Application US/10074978A  
 ; Publication No. US20040010119A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leite, Mario  
 ; APPLICANT: Spytek, Kimberly A  
 ; APPLICANT: Guo, Xiaojia (Sasha)  
 ; APPLICANT: Fernandes, Elma  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Liu, Xiahong  
 ; APPLICANT: Casman, Stacie  
 ; APPLICANT: Boldog, Ferenc  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Blalock, Angela  
 ; APPLICANT: Ballinger, Robert  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Tchernev, Velizar T  
 ; APPLICANT: Malyankar, Uriel M  
 ; APPLICANT: Gusev, Vladimir  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Mezes, Peter S  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Heyes, Melvin P  
 ; APPLICANT: Herrman, John  
 ; APPLICANT: Pena, Carol E A  
 ; APPLICANT: Shimkets, Richard A  
 ; APPLICANT: Taupier Jr, Raymond J  
 ; APPLICANT: Moore, No. US20040010119A1lle  
 ; APPLICANT: Shenoy, Sureeh  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: Gunther, Erik  
 ; APPLICANT: Stone, Dave  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Peyman, John  
 ; APPLICANT: Smithson, Glennda  
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 21402-269  
 ; CURRENT APPLICATION NUMBER: US/10/074,978A  
 ; CURRENT FILING DATE: 2003-01-07  
 ; PRIOR APPLICATION NUMBER: 60/268,221  
 ; PRIOR FILING DATE: 2001-02-12  
 ; PRIOR APPLICATION NUMBER: 60/335,109  
 ; PRIOR FILING DATE: 2001-10-31  
 ; PRIOR APPLICATION NUMBER: 60/312,284  
 ; PRIOR FILING DATE: 2001-08-14  
 ; PRIOR APPLICATION NUMBER: 60/268,496  
 ; PRIOR FILING DATE: 2001-02-13  
 ; PRIOR APPLICATION NUMBER: 60/276,703  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/330,293  
 ; PRIOR FILING DATE: 2001-10-18  
 ; PRIOR APPLICATION NUMBER: 60/322,127  
 ; PRIOR FILING DATE: 2001-11-21  
 ; PRIOR APPLICATION NUMBER: 60/280,899  
 ; PRIOR FILING DATE: 2001-04-02  
 ; PRIOR APPLICATION NUMBER: 60/310,797  
 ; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/268,646  
 ; PRIOR FILING DATE: 2001-02-14  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 547  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 158  
 ; LENGTH: 414  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-10-074-978A-158

Query Match 68.3%; Score 1437.5; DB 15; Length 414;  
 Best Local Similarity 69.7%; Pred. No. 8.6e-113; Indels 19; Gaps 3;  
 Matches 278; Conservative 38; Mismatches 64;  
 QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKCMCKMYMKNQKCV 60  
 DB 1 MGNHSHKPPVFDENEVNFDFEILRAIGKSGFGKVCIVQKRDTKCMYAMKMYMKNQKCV 60  
 QY 61 ERNEVRNVFKELOIMQGLEHPELVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
 DB 61 ERDEVRNVFRELQIMQGLEHPELVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFTE 120  
 QY 121 ETVKLFICELVMDLYLQNRHHRDMKPDNILLDEHGHVHTDFNIAAMLPRETOITTM 180  
 DB 121 GTVKLYICELALAEFLQRYHHRDIKPDNILLDEHGHVHTDFNIAATLVKSGSEKASM 180  
 QY 181 AGTKPYMAPEMFSS--SRKGAGYSFAVDWMSLGVTAAYELLRRGRRPYHRSSTSSKEIVHTF 238  
 DB 181 AGTKPYMADEVFQVYVGGPGYSYPVDMWSLGVTAAYELLRGWRPYEHSATPIDEILNMP 240  
 QY 239 ETVVTPYSANSQEMVSLIKLLEPNPDRFSQSDVQNFYMDINNDVAFQKRLIPG 298  
 DB 241 KVERVHYSWCEGMVSLIKLLEPNPDRFSQSDVQNFYMDINNDVAFQKRLIPG 300  
 QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCILQSHLDSVQK 357  
 DB 301 VFNKGRNLCDPTFELEEMILESPLHKKKKRLAKHSRSDTKDSCLPLNGHLQOCLSTVRK 360  
 QY 358 EPIIFNREKVRNDFNKRQPNLALRQTKDPQSGDQGNL 396  
 DB 361 EPIIFNREKLRQ-----QGHGQLSDL 383

RESULT 12

US-09-801-876B-4  
 ; Sequence 4, Application US/09801876B  
 ; Patent No. US20020127683A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YE, Jane et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; FILE REFERENCE: CL001160  
 ; CURRENT APPLICATION NUMBER: US/09/801,876B  
 ; CURRENT FILING DATE: 2001-03-09  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 404  
 ; TYPE: PRT  
 ; ORGANISM: Mus Musculus  
 ; US-09-801-876B-4

Query Match 67.8%; Score 1427; DB 9; Length 404;  
 Best Local Similarity 69.5%; Pred. No. 6.4e-112;  
 Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;  
 QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKCMCKMYMKNQKCV 60  
 DB 1 MGNHSHKPPVFDENEVNFDFEILRAIGKSGFGKVCIVQKRDTKCMYAMKMYMKNQKCV 60  
 QY 61 -ERNEVRNVFKELOIMQGLEHPELVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 119

Db 61 QERDEVRNPRELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHT 120  
QY 120 EETVKLFICELVMAIDYLNQRIIHRDKPNILLDEHGHVHTDFNIAAMLPRETOITT 179  
Db 121 EGTVKLYICELALALEYLRQTHIHRDIKPNILLDEHGHVHTDFNIAATVKGSEKASS 180  
QY 180 MAGTKPYMAPMFSS--SRKGAGYGFVDVWSLGVTVAYELLGRRPYHRSSTSSKEIVHT 237  
Db 181 MAGTKPYMAPEVQVYVDGGFGYSYPVDWWSLGVTVAYELLGRWPYEHHSATPIDEILNM 240  
QY 238 FETTVVTPSAWSQEMVSLKLLLEPNPDQFSDVQNPFPYNDINWDVAFQKRLIPG 297  
Db 241 FKVERVHYSSTWCEGWSLLKLLTKDPESRLSLRDIQSMYTLADNMWDVAFKALMPG 300  
QY 298 FIPNKGRLNCDPTPELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQSHLSVQ 356  
Db 301 FVPNKGRLNCDPTPELEEMILESPLHKKKRLAKHRSRSTKDCSCPLNGHLQOCLETVR 360  
QY 357 KEPIIFNREKVRNDFNKRQPNLALBQTKDQGEDGQNNNL 396  
Db 361 KEPIIFNREKLRRQ-----QHGDLQSD 384

RESULT 13  
US-10-667-442-4  
; Sequence 4, Application US/10667442  
; Publication No. US2004043466A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160DIV II  
; CURRENT APPLICATION NUMBER: US/10/667,442  
; CURRENT FILING DATE: 2003-09-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-667-442-4

Query Match 67.8%; Score 1427; DB 12; Length 404;  
Best Local Similarity 69.5%; Pred. No. 6.4e-112;  
Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;  
QY 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNNKQCV 60  
Db 1 MGGNHSKPPVFDENEENVDHFDQLRAIGKSGFGEVCIVQKNDTKKMYNNKQCV 60  
QY 61 -ERNEVRNVFKELOIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHT 119  
Db 61 QERDEVRNPRELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHT 120  
QY 120 EETVKLFICELVMAIDYLNQRIIHRDKPNILLDEHGHVHTDFNIAAMLPRETOITT 179  
Db 121 EGTVKLYICELALALEYLRQTHIHRDIKPNILLDEHGHVHTDFNIAATVKGSEKASS 180  
QY 180 MAGTKPYMAPMFSS--SRKGAGYGFVDVWSLGVTVAYELLGRRPYHRSSTSSKEIVHT 237  
Db 181 MAGTKPYMAPEVQVYVDGGFGYSYPVDWWSLGVTVAYELLGRWPYEHHSATPIDEILNM 240  
QY 238 FETTVVTPSAWSQEMVSLKLLLEPNPDQFSDVQNPFPYNDINWDVAFQKRLIPG 297  
Db 241 FKVERVHYSSTWCEGWSLLKLLTKDPESRLSLRDIQSMYTLADNMWDVAFKALMPG 300  
QY 298 FIPNKGRLNCDPTPELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQSHLSVQ 356  
Db 301 FVPNKGRLNCDPTPELEEMILESPLHKKKRLAKHRSRSTKDCSCPLNGHLQOCLETVR 360  
QY 357 KEPIIFNREKVRNDFNKRQPNLALBQTKDQGEDGQNNNL 396

Db 361 KEPIIFNREKLRRQ-----QHGDLQSD 384  
RESULT 14  
US-10-254-869-4  
; Sequence 4, Application US/10254869  
; Publication No. US20030027307A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160DIV  
; CURRENT APPLICATION NUMBER: US/10/254,869  
; CURRENT FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-254-869-4

Query Match 67.8%; Score 1427; DB 14; Length 404;  
Best Local Similarity 69.5%; Pred. No. 6.4e-112;  
Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;  
QY 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNNKQCV 60  
Db 1 MGGNHSKPPVFDENEENVDHFDQLRAIGKSGFGEVCIVQKNDTKKMYNNKQCV 60  
QY 61 -ERNEVRNVFKELOIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHT 119  
Db 61 QERDEVRNPRELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHT 120  
QY 120 EETVKLFICELVMAIDYLNQRIIHRDKPNILLDEHGHVHTDFNIAAMLPRETOITT 179  
Db 121 EGTVKLYICELALALEYLRQTHIHRDIKPNILLDEHGHVHTDFNIAATVKGSEKASS 180  
QY 180 MAGTKPYMAPMFSS--SRKGAGYGFVDVWSLGVTVAYELLGRRPYHRSSTSSKEIVHT 237  
Db 181 MAGTKPYMAPEVQVYVDGGFGYSYPVDWWSLGVTVAYELLGRWPYEHHSATPIDEILNM 240  
QY 238 FETTVVTPSAWSQEMVSLKLLLEPNPDQFSDVQNPFPYNDINWDVAFQKRLIPG 297  
Db 241 FKVERVHYSSTWCEGWSLLKLLTKDPESRLSLRDIQSMYTLADNMWDVAFKALMPG 300  
QY 298 FIPNKGRLNCDPTPELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQSHLSVQ 356  
Db 301 FVPNKGRLNCDPTPELEEMILESPLHKKKRLAKHRSRSTKDCSCPLNGHLQOCLETVR 360  
QY 357 KEPIIFNREKVRNDFNKRQPNLALBQTKDQGEDGQNNNL 396  
Db 361 KEPIIFNREKLRRQ-----QHGDLQSD 384

RESULT 15  
US-09-801-876B-5  
; Sequence 5, Application US/09801876B  
; Patent No. US20020127683A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160  
; CURRENT APPLICATION NUMBER: US/09/801,876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 403

TYPE: PRT  
ORGANISM: Human  
US-09-801-876B-5

Query Match 67.8%; Score 1425.5; DB 9; Length 403;  
Best Local Similarity 68.2%; Pred. No. 8.5e-112;  
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy	1	MGANTSRKPPVPDENSDVNPDPHEILRAIGKSGFGEVCIVQKNDITKMCAMKYMKNQKCV	60
Db	1	MGGNHSHKPPVPDENSDVNPDPHEILRAIGKSGFGEVCIVQKNDITKMCAMKYMKNQKCI	60
Qy	61	ERNEVERNVPKELQIMOGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKS	120
Db	61	ERDEVERNVPKELQIMOGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFTY	120
Qy	121	ETVKLPICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM	180
Db	121	GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVVKABRASSM	180
Qy	181	AGTKPYMAPEMFS--SRKGAGISPAYDWNLSLGVATAYELLGRRPYHIRSTSSKEIVHTF	238
Db	181	AGTKPYMAPEVFOVYMDRPGYSPYDWNLSLGVATAYELLGRWRPYEHSVTPIDEILNMF	240
Qy	239	ETTAVTTPSAWSQEMVSLKLLLEPNPDORFSDVQNPFPYMNNDINWDVAFQKRLIPGF	298
Db	241	KVERVHYSTWCKGMVALLRKLTKDPESRVSSLHDIQSVPLADNWDVAFKALMPGF	300
Qy	299	IPNKGRLNCDPTPELEEMILESXPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK	357
Db	301	VPNKGRLNCDPTPELEEMILESXPLHKKKKRLAKNRSDGTCDSCPLNGHLQHCLETVRE	360
Qy	358	EFIIFNREKVRNDFNKPQPNLALEQTKDPG-----EDGQNNNL	396
Db	361	EFIIFNREKLRQGGQGLDQDTSRGGGQAQSKLQDGCNNNL	403

Search completed: June 25, 2004, 10:56:33  
Job time: 49 secs

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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:48:00 ; Search time 23 Seconds  
(without alignments)  
888.865 Million cell updates/sec

Title: US-10-667-442-2  
Perfect score: 2104  
Sequence: 1 MGNATSRKPPVFDENEDVNF.....NLALRQTKDQGEDQNNL 396

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/6C\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfilees1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	100.0	396	4	US-09-801-876B-2
2	2104	100.0	396	4	US-10-254-869-2
3	2089	99.3	396	4	US-09-841-683-11
4	2047	97.3	407	4	US-09-841-683-9
5	1427	67.8	404	4	US-09-801-876B-4
6	1427	67.8	404	4	US-10-254-869-4
7	1425.5	67.8	403	4	US-09-801-876B-5
8	1425.5	67.8	403	4	US-10-254-869-5
9	1324	62.9	419	4	US-09-799-875-14
10	1317.5	62.6	394	4	US-09-801-876B-6
11	1317.5	62.6	394	4	US-10-254-869-6
12	1378.5	60.8	399	4	US-09-819-607-4
13	1161	55.2	236	4	US-09-841-683-7
14	1158	55.0	225	4	US-09-841-683-5
15	1137.5	54.1	369	4	US-09-819-607-2
16	1122.5	53.4	368	4	US-09-819-607-5
17	1010.5	48.0	316	4	US-09-801-876B-7
18	1010.5	48.0	316	4	US-10-254-869-7
19	843.5	40.1	347	4	US-09-801-876B-8
20	843.5	40.1	347	4	US-10-254-869-8
21	498.5	23.7	336	4	US-09-394-455-2
22	498.5	23.7	343	4	US-09-394-455-15
23	498.5	23.7	343	4	US-09-394-455-34
24	498.5	23.7	351	4	US-09-394-455-4
25	495.5	23.6	587	1	US-08-313-274-2
26	493.5	23.5	689	1	US-08-221-817-18
27	493.5	23.5	689	1	US-08-454-439-18

28 493.5 23.5 689 5 PCT-US94-10487-18 Sequence 18, Appl  
29 492.5 23.4 343 4 US-09-394-455-38 Sequence 38, Appl  
30 492.5 23.4 350 4 US-09-457-040B-37 Sequence 37, Appl  
31 492.5 23.4 351 4 US-09-457-040B-6 Sequence 6, Appl  
32 492.5 23.4 595 4 US-09-417-197-69 Sequence 69, Appl  
33 480.5 22.8 699 1 US-08-221-817-20 Sequence 20, Appl  
34 480.5 22.8 699 1 US-08-454-439-20 Sequence 20, Appl  
35 480.5 22.8 699 5 PCT-US94-10487-20 Sequence 8, Appl  
36 474 22.5 260 2 US-07-857-224B-8 Sequence 8, Appl  
37 473 22.5 260 2 US-07-857-224B-7 Sequence 7, Appl  
38 469.5 22.3 688 1 US-08-221-817-19 Sequence 19, Appl  
39 469.5 22.3 688 1 US-08-454-439-19 Sequence 19, Appl  
40 469.5 22.3 688 5 PCT-US94-10487-19 Sequence 19, Appl  
41 469 22.3 500 1 US-07-980-526-2 Sequence 2, Appl  
42 469 22.3 500 1 US-08-221-817-15 Sequence 15, Appl  
43 469 22.3 500 1 US-08-454-439-15 Sequence 15, Appl  
44 469 22.3 500 4 US-09-614-748A-4 Sequence 4, Appl  
45 469 22.3 500 5 PCT-US94-10487-15 Sequence 15, Appl

## ALIGNMENTS

## RESULT 1

US-09-801-876B-2  
; Sequence 2, Application US/09801876B  
; Patent No. 6492155  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160  
; CURRENT APPLICATION NUMBER: US/09/801,876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Human  
US-09-801-876B-2

Query Match 100.0%; Score 2104; DB 4; Length 396;  
Best Local Similarity 100.0%; Pred. No. 1.6e-194;  
Matches 396, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNATSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKCMKMYMKQKV 60  
Db 1 MGNATSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKCMKMYMKQKV 60  
Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120  
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120  
Qy 121 ETVKLFICELVNDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETIQITM 180  
Db 121 ETVKLFICELVNDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETIQITM 180  
Qy 181 AGTKPYMADEMSSRRKAGYSFVNDWSLGVATYELLRGRPPYHTRSSSTSSKEIVHFT 240  
Db 181 AGTKPYMADEMSSRRKAGYSFVNDWSLGVATYELLRGRPPYHTRSSSTSSKEIVHFT 240  
Qy 241 TVVTTPSAWSQEWVLLKLLPNDQRFSDVQNFPPYMDINNDVAFQKELIPGFIP 300  
Db 241 TVVTTPSAWSQEWVLLKLLPNDQRFSDVQNFPPYMDINNDVAFQKELIPGFIP 300  
Qy 301 NGRNLNCDPTFLEEMILESKPLHKKKGLAKXKDMRKCDSSQTCLLQEHLDVSQKEFI 360  
Db 301 NGRNLNCDPTFLEEMILESKPLHKKKGLAKXKDMRKCDSSQTCLLQEHLDVSQKEFI 360  
Qy 361 IFNRKVRNDFKVRQPNLALRQTKDQGEDQNNL 396  
Db 361 IFNRKVRNDFKVRQPNLALRQTKDQGEDQNNL 396

Db 361 IFNREKVNDRFNKQPNLALEQTKDPOGEDGQNNL 396

## RESULT 2

US-10-254-869-2

; Sequence 2, Application US/10254869

; Patent No. 6653117

; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001160DIV

; CURRENT APPLICATION NUMBER: US/10/254,869

; CURRENT FILING DATE: 2002-09-26

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 396

; TYPE: PRT

; ORGANISM: Human

US-10-254-869-2

Query Match 100.0%; Score 2104; DB 4; Length 396;

Best Local Similarity 100.0%; Pred. No. 1.6e-194;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKKVCV 60

Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKKVCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120

Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120

Qy 121 ETVKLFICELVMDLYLQNRHDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180

Db 121 ETVKLFICELVMDLYLQNRHDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180

Qy 181 AGTKPYMAPFSSRKAGYSPAVDWSLGTAYELLGRPPYHRSSTSSKEIVHTPET 240

Db 181 AGTKPYMAPFSSRKAGYSPAVDWSLGTAYELLGRPPYHRSSTSSKEIVHTPET 240

Qy 241 TVVTYPSAWSQSWSLKLLKLEPNPDORFQSLSDVQNFPPYNDINWDVAFQKRLIPGIP 300

Db 241 TVVTYPSAWSQSWSLKLLKLEPNPDORFQSLSDVQNFPPYNDINWDVAFQKRLIPGIP 300

Qy 301 NKGRLNCDPTFELEEMILESPLHKKKKRLAKKCKDSSQTCLLQEHLDVSQKEFI 360

Db 301 NKGRLNCDPTFELEEMILESPLHKKKKRLAKKCKDSSQTCLLQEHLDVSQKEFI 360

Qy 361 IFNREKVNDRFNKQPNLALEQTKDPOGEDGQNNL 396

Db 361 IFNREKVNDRFNKQPNLALEQTKDPOGEDGQNNL 396

## RESULT 3

US-09-841-683-11

; Sequence 11, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomniichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 396

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-841-683-11

Query Match 99.3%; Score 2089; DB 4; Length 396;

Best Local Similarity 99.5%; Pred. No. 4.4e-193;

Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKKVCV 60

Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCMKMYNKKVCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120

Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120

Qy 121 ETVKLFICELVMDLYLQNRHDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180

Db 121 ETVKLFICELVMDLYLQNRHDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180

Qy 181 AGTKPYMAPFSSRKAGYSPAVDWSLGTAYELLGRPPYHRSSTSSKEIVHTPET 240

Db 181 AGTKPYMAPFSSRKAGYSPAVDWSLGTAYELLGRPPYHRSSTSSKEIVHTPET 240

Qy 241 TVVTYPSAWSQSWSLKLLKLEPNPDORFQSLSDVQNFPPYNDINWDVAFQKRLIPGIP 300

Db 241 TVVTYPSAWSQSWSLKLLKLEPNPDORFQSLSDVQNFPPYNDINWDVAFQKRLIPGIP 300

Qy 301 NKGRLNCDPTFELEEMILESPLHKKKKRLAKKCKDSSQTCLLQEHLDVSQKEFI 360

Db 301 NKGRLNCDPTFELEEMILESPLHKKKKRLAKKCKDSSQTCLLQEHLDVSQKEFI 360

Qy 361 IFNREKVNDRFNKQPNLALEQTKDPOGEDGQNNL 396

Db 361 IFNREKVNDRFNKQPNLALEQTKDPOGEDGQNNL 396

## RESULT 4

US-09-841-683-9

; Sequence 9, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomniichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encodi

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 407

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-841-683-9

Query Match 97.3%; Score 2047; DB 4; Length 407;

Best Local Similarity 98.7%; Pred. No. 5.1e-189;

Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
DB 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
DB 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
QY 121 ETVKLPICELVMDALDYLNQRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 180  
DB 121 ETVKLPICELVMDALDYLNQRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 180  
QY 181 AGTKPYMAPEMPSRRKAGYSFVDMWSLGVATAYELLRRRPPYHRSSTSSKEIVHT 240  
DB 181 AGTKPYMAPEMPSRRKAGYSFVDMWSLGVATAYELLRRRPPYHRSSTSSKEIVHT 240  
QY 241 TVVTYPSAWSQEMVSLKGLLEPNPDQSFQSDVQNFPMYNDINWDVAFQKLLPGFIP 300  
DB 241 TVVTYPSAWSQEMVSLKGLLEPNPDQSFQSDVQNFPMYNDINWDVAFQKLLPGFIP 300  
QY 301 NGRNLCDPTFLEEMILESPLHKKKKLAKKEKDMRKCDSSQTCCLQEHLDVQKQKCV 360  
DB 301 NGRNLCDPTFLEEMILESPLHKKKKLAKKEKDMRKCDSSQTCCLQEHLDVQKQKCV 360  
QY 361 IFNREKVNDRFNKQPNLALEQTKDQGEDGQ 392  
DB 361 IFNREKVNDRFNKQPNLALEQTKDQGVNQG 392

## RESULT 5

US-09-801-876B-4

; Sequence 4, Application US/09801876B

; Patent No. 6492155

; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001160

; CURRENT APPLICATION NUMBER: US/09/801,876B

; CURRENT FILING DATE: 2001-03-09

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Mus Musculus

US-09-801-876B-4

Query Match 67.8%; Score 1427; DB 4; Length 404;

Best Local Similarity 69.5%; Pred. No. 3e-129;

Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
DB 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 119  
DB 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
QY 120 ETVKLPICELVMDALDYLNQRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 179  
DB 120 ETVKLPICELVMDALDYLNQRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 180  
QY 180 MAGTKPYMAPEMPS--SRKAGYSFVDMWSLGVATAYELLRRRPPYHRSSTSSKEIVHT 237  
DB 180 MAGTKPYMAPEVQVYVDDGGPGYSYFVDMWSLGVATAYELLRRRPPYHRSATPDIILNM 240  
QY 238 FETTVVTPYSAWSQEMVSLKGLLEPNPDQSFQSDVQNFPMYNDINWDVAFQKLLPG 297  
DB 241 FKVERVHYSTWCEGMVSLKGLTKDPESSRLSDIQSMYTLADNMWDVAFKALMFG 300

QY 298 FIPNKGRLNCDPTFLEEMILESPLHKKKKLAK-KEKDMRKCDSSQTCCLQEHLDVQ 356  
DB 301 FVPNKGRLNCDPTFLEEMILESPLHKKKKLAKHRSDSTKDCSPLNGHLQOCLETVR 360  
QY 357 KEFIIFNREKVNDRFNKQPNLALEQTKDQGEDGQNNNL 396  
DB 361 KEFIIFNREKLRQ-----QGHGQLSDL 384

## RESULT 6

US-10-254-869-4

; Sequence 4, Application US/10254869

; Patent No. 6653117

; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001160DIV

; CURRENT APPLICATION NUMBER: US/10/254,869

; CURRENT FILING DATE: 2002-09-26

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Mus Musculus

US-10-254-869-4

Query Match 67.8%; Score 1427; DB 4; Length 404;

Best Local Similarity 69.5%; Pred. No. 3e-129;

Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
DB 1 MGNHSHKPPVFDENEVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYMKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 119  
DB 61 QERDEVNRVRELQIMQGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHF 120  
QY 120 ETVKLPICELVMDALDYLNQRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 179  
DB 121 EGTVKLYICELALALEYLQRYHIIHRDKPDNILLDEGHVHITDFNIAATVLKSEKASS 180  
QY 180 MAGTKPYMAPEMPS--SRKAGYSFVDMWSLGVATAYELLRRRPPYHRSSTSSKEIVHT 237  
DB 181 MAGTKPYMAPEVQVYVDDGGPGYSYFVDMWSLGVATAYELLRRRPPYHRSATPDIILNM 240  
QY 238 FETTVVTPYSAWSQEMVSLKGLLEPNPDQSFQSDVQNFPMYNDINWDVAFQKLLPG 297  
DB 241 FKVERVHYSTWCEGMVSLKGLTKDPESSRLSDIQSMYTLADNMWDVAFKALMFG 300  
QY 298 FIPNKGRLNCDPTFLEEMILESPLHKKKKLAK-KEKDMRKCDSSQTCCLQEHLDVQ 356  
DB 301 FVPNKGRLNCDPTFLEEMILESPLHKKKKLAKHRSDSTKDCSPLNGHLQOCLETVR 360  
QY 357 KEFIIFNREKVNDRFNKQPNLALEQTKDQGEDGQNNNL 396  
DB 361 KEFIIFNREKLRQ-----QGHGQLSDL 384

RESULT 7  
US-09-801-876B-5  
; Sequence 5, Application US/09801876B  
; Patent No. 6492155  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160



; CURRENT APPLICATION NUMBER: US/09/801,876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Human  
US-09-801-876B-5

Query Match 67.8%; Score 1425.5; DB 4; Length 403;  
Best Local Similarity 68.2%; Pred. No. 4.1e-129;  
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCKAMKYNKQKCV 60  
DB 1 MGNHSHKPPVFDENEENVDNFDFEILRAIGKSGFGEVCIVQKNDTKKCKAMKYNKQKCI 60  
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFK 120  
DB 61 ERDEVNRVRELOIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFT 120  
QY 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180  
DB 121 GTVKLYICELALALEYLQRYHIIHRDKPDNILLDEHGHVHITDFNIAATVVKGAERASSM 180  
QY 181 AGTKPYMAPEMPS--SRKAGYSFADVWMSLGVTAAYELLRRGRPHYHRSSTSSKEIVHTP 238  
DB 181 AGTKPYMAPEVQVMDRPGYSYPVDMWSLGIATAYELLRGWRPYEHSVTPIDEILNMF 240  
QY 239 ETTVVTVPSAWSQEMVSLKLLPENPDORFSDVQNPFPYMDINWDVAFKRLIPGP 298  
DB 241 KVERVHYSSTCKGVALRLKLTQDPESVSSLDHIOQVPLADNMWDVAFKALMPGP 300  
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSOTCLIQEHLDSVQK 357  
DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKRLAKNRSDGTQKSCPLNGHLQHCLETVRE 360  
QY 358 EFTIFNRKVRNDRFNKRPNALAQTKDPQG-----EDGQNNNL 396  
DB 361 EFTIFNRKLRQQGQSLLDTSRGGGQAQSKLQDGCNNNL 403

## RESULT 8

US-10-254-869-5  
; Sequence 5, Application US/10254869  
; Patent No. 6653117  
; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160DIV  
; CURRENT APPLICATION NUMBER: US/10/254,869  
; CURRENT FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Human

US-10-254-869-5

Query Match 67.8%; Score 1425.5; DB 4; Length 403;  
Best Local Similarity 68.2%; Pred. No. 4.1e-129;  
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCKAMKYNKQKCV 60  
DB 1 MGNHSHKPPVFDENEENVDNFDFEILRAIGKSGFGEVCIVQKNDTKKCKAMKYNKQKCI 60  
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFK 120

DB 61 ERDEVNRVRELOIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFT 120  
QY 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180  
DB 121 GTVKLYICELALALEYLQRYHIIHRDKPDNILLDEHGHVHITDFNIAATVVKGAERASSM 180  
QY 181 AGTKPYMAPEMPS--SRKAGYSFADVWMSLGVTAAYELLRRGRPHYHRSSTSSKEIVHTP 238  
DB 181 AGTKPYMAPEVQVMDRPGYSYPVDMWSLGIATAYELLRGWRPYEHSVTPIDEILNMF 240  
QY 239 ETTVVTVPSAWSQEMVSLKLLPENPDORFSDVQNPFPYMDINWDVAFKRLIPGP 298  
DB 241 KVERVHYSSTCKGVALRLKLTQDPESVSSLDHIOQVPLADNMWDVAFKALMPGP 300  
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSOTCLIQEHLDSVQK 357  
DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKRLAKNRSDGTQKSCPLNGHLQHCLETVRE 360  
QY 358 EFTIFNRKVRNDRFNKRPNALAQTKDPQG-----EDGQNNNL 396  
DB 361 EFTIFNRKLRQQGQSLLDTSRGGGQAQSKLQDGCNNNL 403

## RESULT 9

US-09-799-875-14

; Sequence 14, Application US/09799875  
; Patent No. 6638721

; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses  
; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 35800/209996  
; CURRENT APPLICATION NUMBER: US/09/799,875

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/182,059

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 09/659,287

; PRIOR FILING DATE: 2000-09-12

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens

US-09-799-875-14

Query Match 62.9%; Score 1324; DB 4; Length 419;  
Best Local Similarity 64.5%; Pred. No. 2.7e-119;  
Matches 254; Conservative 53; Mismatches 77; Indels 10; Gaps 4;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCKAMKYNKQKCV 60  
DB 5 MSAATARR-PVFDKEDVNFDFEILRAIGKSGFGEVCIVQKNDTKKCKAMKYNKQKCI 63  
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFK 120  
DB 64 ERDEVNRVRELEIQEIEHVELVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFK 123  
QY 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180  
DB 124 DTVELYICELMALDYLRLGQHIHRDVKPDNILLDEHGHVHITDFNIAATIKOGERATAL 183  
QY 181 AGTKPYMAPEMPS--RKGAGYSFADVWMSLGVTAAYELLRRGRPHYHRSSTSSKEIVHTP 238  
DB 184 AGTKPYMAPEIFHSFVNGGTGYSFVDWMSVGVNAYELLRGWRPYEHSVTPIDEILNMF 243  
QY 239 ETTVVTVPSAWSQEMVSLKLLPENPDORFSDVQNPFPYMDINWDVAFKRLIPGP 298  
DB 244 STVSQVQVPTWSKEMVALLRKLITNFEHLRSLSDVQAPALAGVLDHLSKRVFPGP 303  
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAKKEKDMRKCDSSOT--CLLQEHLSVQ 356

Db 304 VPKGRGLHCDPTFELEEMILESRLPKKKKRLAKNKRSDSSQSENNDYLDCLDAIQ 363  
Qy 357 KEPIFNRKVRNDRPNKQPNALALQTKDPQGED 390  
Db 364 QDFVIFNRKL-----KRSQDLPREPLPAPESRD 392

RESULT 10  
US-09-801-876B-6  
; Sequence 6, Application US/09801876B  
; Patent No. 6492155  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-09-801-876B-6

Query Match 62.6%; Score 1317.5; DB 4; Length 384;  
Best Local Similarity 64.3%; Pred. No. 9.9e-119;  
Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 3;  
Qy 6 SRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYNNKQKVERNEV 65  
Db 1 SARPPVFDKEDVNFDFHFOILRAIGKSGFKVCIVQKRDTEKMYAMKYNKQCCIERDEV 60  
Qy 66 RNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKL 125  
Db 61 RNVFRELILQIEHVFVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVQFSEDVRL 120  
Qy 126 FICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHTDNIAMLPRETOITTMAGTKP 185  
Db 121 YICEMALALDYLRSHQIHRDVKPDNILLDEQGHHLTDFNIATIIKDGERTALAGTKP 180  
Qy 186 YMPEMFSS--RKAGYSFADVMSLGYTAYELLGRPPYHIRSTSSKEIVHFPETTV 243  
Db 181 YMPEIFHSFVNGGTGYSFVDWMSVGMAYELLGRPPYDIHSSNAVESLVQLFSTVSV 240  
Qy 244 TYPASQEMVSLKLLLEPNPDRFSQSDVQNPFPYMDINWDVAFQKRLIPGPIPNKG 303  
Db 241 QYVPTWSKEMVALLRKLITVNPHEHRSFSLQDMQTAPSLAHVLDLSEKKVPGFVPNGK 300  
Qy 304 RLNCPTFELEEMILESPLHKKKRLAKKEKMDKCDSSQT--CLLOEHLDSVQKEFII 361  
Db 301 RLHCDPTFELEEMILESRLPKKKKRLAKNKRSDSSQSENNDYLDCLDAIQDFVI 360  
Qy 362 FNRKVNDRFNRKQPNLALQTKDPQGED 390  
Db 361 FNRKEL-----KRSQELMSEPPPGPETSD 384

RESULT 11  
US-10-254-869-6  
; Sequence 6, Application US/10254869  
; Patent No. 6653117  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160DIV  
; CURRENT FILING DATE: 2002-09-26

; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-254-869-6

Query Match 62.6%; Score 1317.5; DB 4; Length 384;  
Best Local Similarity 64.3%; Pred. No. 9.9e-119;  
Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 3;  
Qy 6 SRKPPVFDENEDVNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYNNKQKVERNEV 65  
Db 1 SARPPVFDKEDVNFDFHFOILRAIGKSGFKVCIVQKRDTEKMYAMKYNKQCCIERDEV 60  
Qy 66 RNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKL 125  
Db 61 RNVFRELILQIEHVFVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVQFSEDVRL 120  
Qy 126 FICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHTDNIAMLPRETOITTMAGTKP 185  
Db 121 YICEMALALDYLRSHQIHRDVKPDNILLDEQGHHLTDFNIATIIKDGERTALAGTKP 180  
Qy 186 YMPEMFSS--RKAGYSFADVMSLGYTAYELLGRPPYHIRSTSSKEIVHFPETTV 243  
Db 181 YMPEIFHSFVNGGTGYSFVDWMSVGMAYELLGRPPYDIHSSNAVESLVQLFSTVSV 240  
Qy 244 TYPASQEMVSLKLLLEPNPDRFSQSDVQNPFPYMDINWDVAFQKRLIPGPIPNKG 303  
Db 241 QYVPTWSKEMVALLRKLITVNPHEHRSFSLQDMQTAPSLAHVLDLSEKKVPGFVPNGK 300  
Qy 304 RLNCPTFELEEMILESPLHKKKRLAKKEKMDKCDSSQT--CLLOEHLDSVQKEFII 361  
Db 301 RLHCDPTFELEEMILESRLPKKKKRLAKNKRSDSSQSENNDYLDCLDAIQDFVI 360  
Qy 362 FNRKVNDRFNRKQPNLALQTKDPQGED 390  
Db 361 FNRKEL-----KRSQELMSEPPPGPETSD 384

RESULT 12  
US-09-819-607-4  
; Sequence 4, Application US/09819607  
; Patent No. 6686176  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001078  
; CURRENT APPLICATION NUMBER: US/09/819,607  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 399  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-819-607-4

Query Match 60.8%; Score 1278.5; DB 4; Length 399;  
Best Local Similarity 64.5%; Pred. No. 6e-115;  
Matches 243; Conservative 52; Mismatches 73; Indels 9; Gaps 3;  
Qy 18 VNFDFEILRAIGKSGFGEVCIQKNDTKKCMKMYNNKQKVERNEVNFVKELQIMQ 77  
Db 1 VNFDFHFOILRAIGKSGFKVCIVQKRDTEKMYAMKYNKQCCIERDEVNFVRELEILQE 60  
Qy 78 LEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKLFICELVMALDY 137  
Db 61 IEHVFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVQFSEDVRLYICEMALALDY 120



